BEST AVAILABLE IMAGES

Defective images within this document are accurate representation of The original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

As rescanning documents *will not* correct images, please do not report the images to the Image Problem Mailbox.

Figure 1

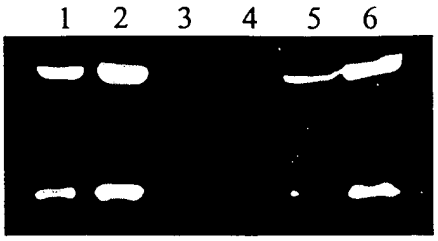

Figure 2

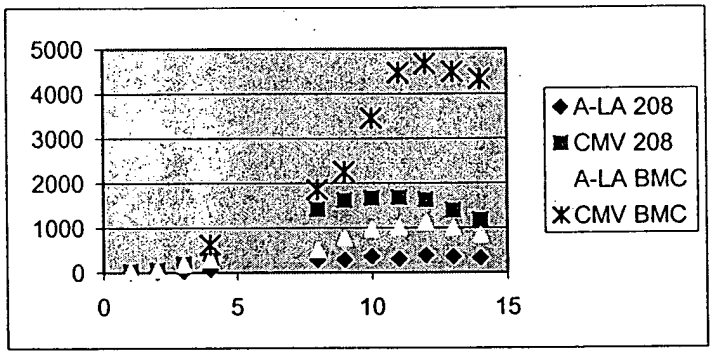

Figure 3

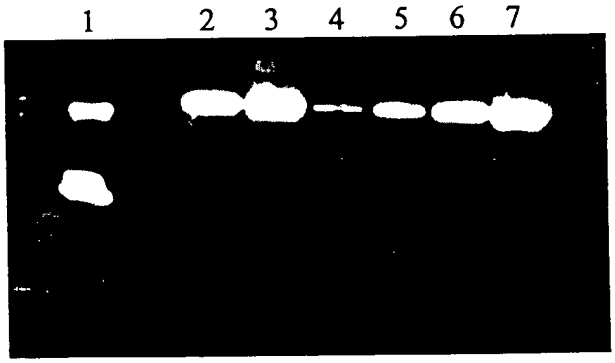

Figure 4
SEQ ID NO:1
Hybrid Human-Bovine Alpha-Lactalbumin Promoter

```
1     GATCAGTCCTGGGTGGTCATTGAAAGGACTGATGCTGAAGTTGAAGCTCC
51    AATACTTTGGCCACCTGATGCGAAGAACTGACTCATGTGATAAGACCCTG
101   ATACTGGGAAAGATTGAAGGCAGGAGGAGAAGGGATGACAGAGGATGGAA
151   GAGTTGGATGGAATCACCAACTCGATGGACATGAGTTTGAGCAAGCTTCC
201   AGGAGTTGGTAATGGGCAGGGAAGCCTGGCGTGCTGCAGTCCATGGGGTT
251   GCAAAGAGTTGGACACTACTGAGTGACTGAACTGAACTGATAGTGTAATC
301   CATGGTACAGAATATAGGATAAAAAAGAGGAAGAGTTTGCCCTGATTCTG
351   AAGAGTTGTAGGATATAAAAGTTTAGAATACCTTTAGTTTGGAAGTCTTA
401   AATTATTTACTTAGGATGGGTACCCACTGCAATATAAGAAATCAGGCTTT
451   AGAGACTGATGTAGAGAGAATGAGCCCTGGCATACCAGAAGCTAACAGCT
501   ATTGGTTATAGCTGTTATAACCAATATATAACCAATATATTGGTTATATA
551   GCATGAAGCTTGATGCCAGCAATTTGAAGGAACCATTTAGAACTAGTATC
601   CTAAACTCTACATGTTCCAGGACACTGATCTTAAAGCTCAGGTTCAGAAT
651   CTTGTTTTATAGGCTCTAGGTGTATATTGTGGGGCTTCCCTGGTGGCTCA
701   GATGGTAAAGTGTCTGCCTGCAATGTGGGTGATCTGGGTTCGATCCCTGG
751   CTTGGGAAGATCCCCTGGAGAAGGAAATGGCAACCCACTCTAGTACTCTT
801   ACCTGGAAAATTCCATGGACAGAGGAGCCTTGTAAGCTACAGTCCATGGG
851   ATTGCAAAGAGTTGAACACAACTGAGCAACTAAGCACAGCACAGTACAGT
900   ATACACCTGTGAGGTGAAGTGAAGTGAAGGTTCAATGCAGGGTCTCCTGC
951   ATTGCAGAAAGATTCTTTACCATCTGAGCCACCAGGGAAGCCCAAGAATA
1001  CTGGAGTGGGTAGCCTATTCCTTCTCCAGGGGATCTTCCCATCCCAGGAA
1051  TTGAACTGGAGTCTCCTGCATTTCAGGTGGATTCTTCACCAGCTGAACTA
1101  CCAGGTGGATACTACTCCAATATTAAAGTGCTTAAAGTCCAGTTTTCCCA
1151  CCTTTCCCAAAAAGGTTGGGTCACTCTTTTTTAACCTTCTGTGGCCTACT
1201  CTGAGGCTGTCTACAAGCTTATATATTTATGAACACATTTATTGCAAGTT
1251  GTTAGTTTTAGATTTACAATGTGGTATCTGGCTATTTAGTGGTATTGGTG
1301  GTTGGGGATGGGGAGGCTGATAGCATCTCAGAGGGCAGCTAGATACTGTC
1351  ATACACACTTTTCAAGTTCTCCATTTTTGTGAAATAGAAAGTCTCTGGAT
1401  CTAAGTTATATGTGATTCTCAGTCTCTGTGGTCATATTCTATTCTACTCC
1451  TGACCACTCAACAAGGAACCAAGATATCAAGGGACACTTGTTTTGTTTCA
1501  TGCCTGGGTTGAGTGGGCCATGACATATGTTCTGGGCCTTGTTACATGGC
1551  TGGATTGGTTGGACAAGTGCCAGCTCTGATCCTGGGACTGTGGCATGTGA
1601  TGACATACACCCCCTCTCCACATTCTGCATGTCTCTAGGGGGGAAGGGGG
1651  AAGCTCGGTATAGAACCTTTATTGTATTTTCTGATTGCCTCACTTCTTAT
1701  ATTGCCCCCATGCCCTTCTTTGTTCCTCAAGTAACCAGAGACAGTGCTTC
1751  CCAGAACCAACCCTACAAGAAACAAAGGGCTAAACAAAGCCAAATGGGAA
1801  GCAGGATCATGGTTTGAACTCTTTCTGGCCAGAGAACAATACCTGCTATG
1851  GACTAGATACTGGGAGAGGGAAAGGAAAAGTAGGGTGAATTATGGAAGGA
1901  AGCTGGCAGGCTCAGCGTTTCTGTCTTGGCATGACCAGTCTCTCTTCATT
1951  CTCTTCCTAGATGTAGGGCTTGGTACCAGAGCCCCTGAGGCTTTCTGCAT
2001  GAATATAAATATATGAAACTGAGTGATGCTTCCATTTCAGGTTCTTGGGG
2051  GCGCCGAATTCGAGCTCGGTACCCGGGGATCTCGAGGGGGGGCCCGGTAC
2101  C
```

1 - 1525	Bovine alpha lactalbumin 5' flanking region (-2000 to -550 from the bovine alpha-lactalbumin transcription start point)
1526 - 2056	Human alpha-lactalbumin 5' flanking region (-600 to +15 from the human alpha-lactalbumin transcription start point)
2057 - 2101	Multiple cloning site

Figure 5
SEQ ID NO:2
Mutated PPE Sequence

```
1       GATTACTTACTGGCAGGTGCTGGGGGCTTCCGAGACAATCGCGAACATCT
51      ACACCACACAACACCGCCTCGACCAGGGTGAGATATCGGCCGGGGACGCG
101     GCGGTGGTAATTACAAGCGAGGATCCGATTACTTACTGGCAGGTGCTGGG
151     GGCTTCCGAGACAATCGCGAACATCTACACCACACAACACCGCCTCGACC
201     AGGGTGAGATATCGGCCGGGGACGCGGCGGTGGTAATTACAAGCG
```

1 - 119	Mutated PPE
120 -126	Linker
127 - 245	Mutated PPE

Figure 6
SEQ ID NO:3
IRES-Signal Peptide Sequence

```
1      GGAATTCGCCCCTCTCCCTCCCCCCCCCCTAACGTTACTGGCCGAAGCCG
51     CTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTATTTTCCACCATAT
101    TGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCTGTCTTCTTG
151    ACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGAATGCAAGGTCT
201    GTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAAA
251    CAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCCCCACCTGGCGAC
301    AGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAAGGC
351    GGCACAACCCCAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGAGTCA
401    AATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCCAGAAG
451    GTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTGCACATGCTTTAC
501    ATGTGTTTAGTCGAGGTTAAAAAAACGTCTAGGCCCCCCGAACCACGGGG
551    ACGTGGTTTTCCTTTGAAAAACACGATGATAATATGGCCTCCTTTGTCTC
601    TCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCCGGCGCCATGG
651    GATATCTAGATCTCGAGCTCGCGAAAGCTT
```

1 - 583	IRES
584 - 640	Modified bovine alpha-lactalbumin signal peptide coding region
641 - 680	Multiple cloning site

Figure 7a
SEQ ID NO:4
CMV MN14 Vector

```
1       CGGATCCGGCCATTAGCCATATTATTCATTGGTTATATAGCATAAATCAA
51      TATTGGCTATTGGCCATTGCATACGTTGTATCCATATCATAATATGTACA
101     TTTATATTGGCTCATGTCCAACATTACCGCCATGTTGACATTGATTATTG
151     ACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATA
201     TATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGAC
251     CGCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATA
301     GTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACG
351     GTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGC
401     CCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAG
451     TACATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGT
501     CATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTG
551     GATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTC
601     AATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCG
651     TAACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCATGTACGGTGGG
701     AGGTCTATATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCGCCTGGAGA
751     CGCCATCCACGCTGTTTTGACCTCCATAGAAGACACCGGGACCGATCCAG
801     CCTCCGCGGCCCCAAGCTTCTCGACGGATCCCCGGGAATTCAGGACCTCA
851     CCATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGT
901     GTCCACTCCGAGGTCCAACTGGTGGAGAGCGGTGGAGGTGTTGTGCAACC
951     TGGCCGGTCCCTGCGCCTGTCCTGCTCCGCATCTGGCTTCGATTTCACCA
1001    CATATTGGATGAGTTGGGTGAGACAGGCACCTGGAAAAGGTCTTGAGTGG
1051    ATTGGAGAAATTCATCCAGATAGCAGTACGATTAACTATGCGCCGTCTCT
1101    AAAGGATAGATTTACAATATCGCGAGACAACGCCAAGAACACATTGTTCC
1151    TGCAAATGGACAGCCTGAGACCCGAAGACACCGGGGTCTATTTTTGTGCA
1201    AGCCTTTACTTCGGCTTCCCCTGGTTTGCTTATTGGGGCCAAGGGACCCC
1251    GGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGG
1301    CACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTG
1351    GTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGC
1401    CCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGAC
1451    TCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
1501    CAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGA
1551    CAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGT
1601    GCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCA
1651    AAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGT
1701    GGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACG
1751    TGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG
1801    TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGA
1851    CTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCC
1901    CAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAA
1951    CCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCA
2001    GGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCG
2051    TGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT
2101    CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGT
2151    GGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGC
2201    ACGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCC
2251    GGGAAATGAAAGCCGAATTCGCCCCTCTCCCTCCCCCCCCCCTAACGTTA
2301    CTGGCCGAAGCCGCTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTA
2351    TTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGG
2401    CCCTGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAG
2451    GAATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCT
2501    TCTTGAAGACAAACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCC
2551    CCCACCTGGCGACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATA
2601    CACCTGCAAAGGCGGCACAACCCCAGTGCCACGTTGTGAGTTGGATAGTT
2651    GTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAA
2701    GGATGCCCAGAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGT
2751    GCACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAAACGTCTAGGCCCC
2801    CCGAACCACGGGGACGTGGTTTTCCTTTGAAAAACACGATGATAATATGG
```

Figure 7b

```
2851  CCTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAG
2901  GCCGACATCCAGCTGACCCAGAGCCCAAGCAGCCTGAGCGCCAGCGTGGG
2951  TGACAGAGTGACCATCACCTGTAAGGCCAGTCAGGATGTGGGTACTTCTG
3001  TAGCCTGGTACCAGCAGAAGCCAGGTAAGGCTCCAAAGCTGCTGATCTAC
3051  TGGACATCCACCCGGCACACTGGTGTGCCAAGCAGATTCAGCGGTAGCGG
3101  TAGCGGTACCGACTTCACCTTCACCATCAGCAGCCTCCAGCCAGAGGACA
3151  TCGCCACCTACTACTGCCAGCAATATAGCCTCTATCGGTCGTTCGGCCAA
3201  GGGACCAAGGTGGAAATCAAACGAACTGTGGCTGCACCATCTGTCTTCAT
3251  CTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT
3301  GCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTG
3351  GATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA
3401  CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAG
3451  CAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGC
3501  CTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAGATC
3551  TAGGCCTCCTAGGTCGACATCGATAAAATAAAAGATTTTATTTAGTCTCC
3601  AGAAAAAGGGGGGAATGAAAGACCCCACCTGTAGGTTTGGCAAGCTAGCT
3651  TAAGTAACGCCATTTTGCAAGGCATGGAAAAATACATAACTGAGAATAGA
3701  GAAGTTCAGATCAAGGTCAGGAACAGATGGAACAGCTGAATATGGGCCAA
3751  ACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACA
3801  GATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTC
3851  CTGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCAGCC
3901  CTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAAGGAC
3951  CTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTCGCTTCTCG
4001  CTTCTGTTCGCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCCACAAC
4051  CCCTCACTCGGGGCGCCAGTCCTCCGATTGACTGAGTCGCCCGGGTACCC
4101  GTGTATCCAATAAACCCTCTTGCAGTTGCATCCGACTTGTGGTCTCGCTG
4151  TTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGGGGTC
4201  TTTCATT
```

1 - 812	CMV promoter/enhancer
853-855	MN14 antibody heavy chain gene signal peptide start codon
2257 - 2259	MN14 antibody heavy chain gene start codon
2271 - 2846	EMCV IRES
2847 - 2849	Bovine alpha-lactalbumin signal peptide start codon
2904 - 2906	First codon mature MN14 antibody light chain gene
3543 - 3544	MN14 antibody light chain gene stop codon
3614 - 4207	MoMuLV 3' LTR

Figure 8a
SEQ ID NO:5
CMV LL2 Vector

1	GGATCCGGCCATTAGCCATATTATTCATTGGTTATATAGCATAAATCAAT
51	ATTGGCTATTGGCCATTGCATACGTTGTATCCATATCATAATATGTACAT
101	TTATATTGGCTCATGTCCAACATTACCGCCATGTTGACATTGATTATTGA
151	CTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATAT
201	ATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACC
251	GCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAG
301	TAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGG
351	TAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCC
401	CCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGT
451	ACATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTC
501	ATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGG
551	ATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCA
601	ATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGT
651	AACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCATGTACGGTGGGA
701	GGTCTATATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCGCCTGGAGAC
751	GCCATCCACGCTGTTTTGACCTCCATAGAAGACACCGGGACCGATCCAGC
801	CTCCGCGGCCCCAAGCTTCTCGACGGATCCCCGGGAATTCAGGACCTCAC
851	CATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTG
901	TCCACTCCCAGGTCCAGCTGGTCCAATCAGGGGCTGAAGTCAAGAAACCT
951	GGGTCATCAGTGAAGGTCTCCTGCAAGGCTTCTGGCTACACCTTTACTAG
1001	CTACTGGCTGCACTGGGTCAGGCAGGCACCTGGACAGGGTCTGGAATGGA
1051	TTGGATACATTAATCCTAGGAATGATTATACTGAGTACAATCAGAACTTC
1101	AAGGACAAGGCCACAATAACTGCAGACGAATCCACCAATACAGCCTACAT
1151	GGAGCTGAGCAGCCTGAGGTCTGAGGACACGGCATTTTATTTTTGTGCAA
1201	GAAGGGATATTACTACGTTCTACTGGGGCCAAGGCACCACGGTCACCGTC
1251	TCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTC
1301	CAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACT
1351	ACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGC
1401	GGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCT
1451	CAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACA
1501	TCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTT
1551	GAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACC
1601	TGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGG
1651	ACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGAC
1701	GTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGT
1751	GGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCA
1801	CGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT
1851	GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCAT
1901	CGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
1951	ACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTG
2001	ACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGA
2051	GAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGG
2101	ACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGC
2151	AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCACGAGGCTCT
2201	GCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCCGGGAAATGAA
2251	AGCCGAATTCGCCCCTCTCCCTCCCCCCCCCCTAACGTTACTGGCCGAAG
2301	CCGCTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTATTTTCCACCA
2351	TATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCTGTCTTC
2401	TTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGAATGCAAGG
2451	TCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGAC
2501	AAACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCCCCACCTGGC
2551	GACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAA
2601	GGCGGCACAACCCCAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGAG
2651	TCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCCAG
2701	AAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTGCACATGCTT
2751	TACATGTGTTTAGTCGAGGTTAAAAAAACGTCTAGGCCCCCCGAACCACG
2801	GGGACGTGGTTTTCCTTTGAAAAACACGATGATAATATGGCCTCCTTTGT

Figure 8b

```
2851  CTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCCGACATCC
2901  AGCTGACCCAGTCTCCATCATCTCTGAGCGCATCTGTTGGAGATAGGGTC
2951  ACTATGAGCTGTAAGTCCAGTCAAAGTGTTTTATACAGTGCAAATCACAA
3001  GAACTACTTGGCCTGGTACCAGCAGAAACCAGGGAAAGCACCTAAACTGC
3051  TGATCTACTGGGCATCCACTAGGGAATCTGGTGTCCCTTCGCGATTCTCT
3101  GGCAGCGGATCTGGGACAGATTTTACTTTCACCATCAGCTCTCTTCAACC
3151  AGAAGACATTGCAACATATTATTGTCACCAATACCTCTCCTCGTGGACGT
3201  TCGGTGGAGGGACCAAGGTGCAGATCAAACGAACTGTGGCTGCACCATCT
3251  GTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTC
3301  TGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGT
3351  GGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACA
3401  GAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCT
3451  GAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCC
3501  ATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT
3551  TAGAGATCTAGGCCTCCTAGGTCGACATCGATAAAATAAAAGATTTTATT
3601  TAGTCTCCAGAAAAAGGGGGGAATGAAAGACCCCACCTGTAGGTTTGGCA
3651  AGCTAGCTTAAGTAACGCCATTTTGCAAGGCATGGAAAAATACATAACTG
3701  AGAATAGAGAAGTTCAGATCAAGGTCAGGAACAGATGGAACAGCTGAATA
3751  TGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGC
3801  CAAGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTA
3851  AGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCG
3901  GTCCAGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCC
3951  CCAAGGACCTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTC
4001  GCTTCTCGCTTCTGTTCGCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAG
4051  CCCACAACCCCTCACTCGGGGCGCCAGTCCTCCGATTGACTGAGTCGCCC
4101  GGGTACCCGTGTATCCAATAAACCCTCTTGCAGTTGCATCCGACTTGTGG
4151  TCTCGCTGTTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAG
4201  GTCTTTCATT
```

1 - 812	CMV promoter/enhancer
852 - 854	LL2 antibody heavy chain signal peptide start codon
2247 - 2249	LL2 antibody heavy chain stop codon
2261 - 2836	EMCV IRES
2837 - 2839	Bovine alpha-lactalbumin signal peptide start codon
2894-2896	First codon of mature LL2 antibody light chain gene
3551 - 3553	LL2 antibody light chain gene stop codon
3622 - 4210	MoMuLV 3' LTR

Figure 9a
SEQ ID NO:6
MMTV MN14 Vector

```
1     CGAGCTTGGCAGAAATGGTTGAACTCCCGAGAGTGTCCTACACCTAGGGG
51    AGAAGCAGCCAAGGGGTTGTTTCCCACCAAGGACGACCCGTCTGCGCACA
101   AACGGATGAGCCCATCAGACAAAGACATATTCATTCTCTGCTGCAAACTT
151   GGCATAGCTCTGCTTTGCCTGGGGCTATTGGGGGAAGTTGCGGTTCGTGC
201   TCGCAGGGCTCTCACCCTTGACTCTTTCAATAATAACTCTTCTGTGCAAG
251   ATTACAATCTAAACAATTCGGAGAACTCGACCTTCCTCCTGAGGCAAGGA
301   CCACAGCCAACTTCCTCTTACAAGCCGCATCGATTTTGTCCTTCAGAAAT
351   AGAAATAAGAATGCTTGCTAAAAATTATATTTTTACCAATAAGACCAATC
401   CAATAGGTAGATTATTAGTTACTATGTTAAGAAATGAATCATTATCTTTT
451   AGTACTATTTTTACTCAAATTCAGAAGTTAGAAATGGGAATAGAAAATAG
501   AAAGAGACGCTCAACCTCAATTGAAGAACAGGTGCAAGGACTATTGACCA
551   CAGGCCTAGAAGTAAAAAAGGGAAAAAAGAGTGTTTTTGTCAAAATAGGA
601   GACAGGTGGTGGCAACCAGGGACTTATAGGGGACCTTACATCTACAGACC
651   AACAGATGCCCCCTTACCATATACAGGAAGATATGACTTAAATTGGGATA
701   GGTGGGTTACAGTCAATGGCTATAAAGTGTTATATAGATCCCTCCCCTTT
751   CGTGAAAGACTCGCCAGAGCTAGACCTCCTTGGTGTATGTTGTCTCAAGA
801   AAAGAAAGACGACATGAAACAACAGGTACATGATTATATTTATCTAGGAA
851   CAGGAATGCACTTTTGGGGAAAGATTTTCCATACCAAGGAGGGGACAGTG
901   GCTGGACTAATAGAACATTATTCTGCAAAAACTTATGGCATGAGTTATTA
951   TGATTAGCCTTGATTTGCCCAACCTTGCGGTTCCCAAGGCTTAAGTAAGT
1001  TTTTGGTTACAAACTGTTCTTAAAACAAGGATGTGAGACAAGTGGTTTCC
1051  TGACTTGGTTTGGTATCAAAGGTTCTGATCTGAGCTCTGAGTGTTCTATT
1101  TTCCTATGTTCTTTTGGAATTTATCCAAATCTTATGTAAATGCTTATGTA
1151  AACCAAGATATAAAAGAGTGCTGATTTTTTGAGTAAACTTGCAACAGTCC
1201  TAACATTCACCTCTTGTGTGTTTGTGTCTGTTCGCCATCCCGTCTCCGCT
1251  CGTCACTTATCCTTCACTTTCCAGAGGGTCCCCCCGCAGACCCCGGCGAC
1301  CCTCAGGTCGGCCGACTGCGGCAGCTGGCGCCCGAACAGGGACCCTCGGA
1351  TAAGTGACCCTTGTCTTTATTTCTACTATTTTGTGTTCGTCTTGTTTTGT
1401  CTCTATCTTGTCTGGCTATCATCACAAGAGCGGAACGGACTCACCTCAGG
1451  GAACCAAGCTAGCCCGGGGTCGACGGATCCGATTACTTACTGGCAGGTGC
1501  TGGGGGCTTCCGAGACAATCGCGAACATCTACACCACACAACACCGCCTC
1551  GACCAGGGTGAGATATCGGCCGGGGACGCGGCGGTGGTAATTACAAGCGA
1601  GATCCGATTACTTACTGGCAGGTGCTGGGGGCTTCCGAGACAATCGCGAA
1651  CATCTACACCACACAACACCGCCTCGACCAGGGTGAGATATCGGCCGGGG
1701  ACGCGGCGGTGGTAATTACAAGCGAGATCCCCGGGAATTCAGGACCTCAC
1751  CATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTG
1801  TCCACTCCGAGGTCCAACTGGTGGAGAGCGGTGGAGGTGTTGTGCAACCT
1851  GGCCGGTCCCTGCGCCTGTCCTGCTCCGCATCTGGCTTCGATTTCACCAC
1901  ATATTGGATGAGTTGGGTGAGACAGGCACCTGGAAAAGGTCTTGAGTGGA
1951  TTGGAGAAATTCATCCAGATAGCAGTACGATTAACTATGCGCCGTCTCTA
2001  AAGGATAGATTTACAATATCGCGAGACAACGCCAAGAACACATTGTTCCT
2051  GCAAATGGACAGCCTGAGACCCGAAGACACCGGGGTCTATTTTTGTGCAA
2101  GCCTTTACTTCGGCTTCCCCTGGTTTGCTTATTGGGGCCAAGGGACCCCG
2151  GTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC
2201  ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGG
2251  TCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCC
2301  CTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACT
2351  CTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCC
2401  AGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGAC
2451  AAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTG
2501  CCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAA
2551  AACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTG
2601  GTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGT
2651  GGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGT
2701  ACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGAC
2751  TGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCC
2801  AGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAAC
```

APPROVED BY DRAFTSMAN	O.G. FIG.	
	CLASS	SUBCLASS

Figure 9b

2851 CACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAG
2901 GTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGT
2951 GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTC
3001 CCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTG
3051 GACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCA
3101 CGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCCG
3151 GGAAATGAAAGCCGAATTCGCCCCTCTCCCTCCCCCCCCCCTAACGTTAC
3201 TGGCCGAAGCCGCTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTAT
3251 TTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGC
3301 CCTGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGG
3351 AATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTT
3401 CTTGAAGACAAACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCC
3451 CCACCTGGCGACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATAC
3501 ACCTGCAAAGGCGGCACAACCCCAGTGCCACGTTGTGAGTTGGATAGTTG
3551 TGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAG
3601 GATGCCCAGAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTG
3651 CACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAAACGTCTAGGCCCCC
3701 CGAACCACGGGGACGTGGTTTTCCTTTGAAAAACACGATGATAATATGGC
3751 CTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGG
3801 CCGACATCCAGCTGACCCAGAGCCCAAGCAGCCTGAGCGCCAGCGTGGGT
3851 GACAGAGTGACCATCACCTGTAAGGCCAGTCAGGATGTGGGTACTTCTGT
3901 AGCCTGGTACCAGCAGAAGCCAGGTAAGGCTCCAAAGCTGCTGATCTACT
3951 GGACATCCACCCGGCACACTGGTGTGCCAAGCAGATTCAGCGGTAGCGGT
4001 AGCGGTACCGACTTCACCTTCACCATCAGCAGCCTCCAGCCAGAGGACAT
4051 CGCCACCTACTACTGCCAGCAATATAGCCTCTATCGGTCGTTCGGCCAAG
4101 GGACCAAGGTGGAAATCAAACGAACTGTGGCTGCACCATCTGTCTTCATC
4151 TTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTG
4201 CCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGG
4251 ATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGAC
4301 AGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGC
4351 AGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCC
4401 TGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAGATCC
4451 CCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATAATCAACCTCTGGA
4501 TTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTT
4551 TTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCT
4601 TCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTGCTGTC
4651 TCTTTATGAGGAGTTGTGGCCCGTTGTCAGGCAACGTGGCGTGGTGTGCA
4701 CTGTGTTTGCTGACGCAACCCCCACTGGTTGGGGCATTGCCACCACCTGT
4751 CAGCTCCTTTCCGGGACTTTCGCTTTCCCCCTCCCTATTGCCACGGCGGA
4801 ACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGG
4851 GCACTGACAATTCCGTGGTGTTGTCGGGGAAATCATCGTCCTTTCCTTGG
4901 CTGCTCGCCTGTGTTGCCACCTGGATTCTGCGCGGGACGTCCTTCTGCTA
4951 CGTCCCTTCGGCCCTCAATCCAGCGGACCTTCCTTCCCGCGGCCTGCTGC
5001 CGGCTCTGCGGCCTCTTCCGCGTCTTCGCCTTCGCCCTCAGACGAGTCGG
5051 ATCTCCCTTTGGGCCGCCTCCCCGCCTGATCGATACCGTCAACATCGATA
5101 AAATAAAAGATTTTATTTAGTCTCCAGAAAAAGGGGGGAATGAAAGACCC
5151 CACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGCAAGGCAT
5201 GGAAAAATACATAACTGAGAATAGAGAAGTTCAGATCAAGGTCAGGAACA
5251 GATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTC
5301 CTGCCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGGCCAA
5351 ACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACA
5401 GATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGAGAACCATCA
5451 GATGTTTCCAGGGTGCCCCAAGGACCTGAAATGACCCTGTGCCTTATTTG
5501 AACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCTTCTGCTCCC
5551 CGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGGGCGCCAGTCCTCC
5601 GATTGACTGAGTCGCCCGGGTACCCGTGTATCCAATAAACCCTCTTGCAG
5651 TTGCATCCGACTTGTGGTCTCGCTGTTCCTTGGGAGGGTCTCCTCTGAGT
5701 GATTGACTACCCGTCAGCGGGGGTCTTTCATT

1 - 1457 Mouse mammary tumor virus LTR
1475 - 1726 Double mutated PPE sequence

Figure 9c

1752 - 1754	MN14 heavy chain signal peptide start codon
3156 - 3158	MN14 heavy chain stop codon
3170 - 3745	EMCV IRES
3746 - 3748	Bovine alpha-lactalbumin signal peptide start codon
3803 - 3805	First codon of mature MN14 light chain gene
4442 - 4444	MN14 antibody light chain gene stop codon
4487 - 5078	WPRE sequence
5133 - 5372	MoMuLV 3' LTR

Figure 10a
SEQ ID NO:7
Alpha-Lactalbumin MN14 Vector

```
1     AAAGACCCCACCCGTAGGTGGCAAGCTAGCTTAAGTAACGCCACTTTGCA
51    AGGCATGGAAAAATACATAACTGAGAATAGAAAAGTTCAGATCAAGGTCA
101   GGAACAAAGAAACAGCTGAATACCAAACAGGATATCTGTGGTAAGCGGTT
151   CCTGCCCCGGCTCAGGGCCAAGAACAGATGAGACAGCTGAGTGATGGGCC
201   AAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCGGGGCCAAGAA
251   CAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGTGAATCAT
301   CAGATGTTTCCAGGGTGCCCCAAGGACCTGAAAATGACCCTGTACCTTAT
351   TTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCTTCCGCT
401   CTCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGCGCGCCAGTCT
451   TCCGATAGACTGCGTCGCCCGGGTACCCGTATTCCCAATAAAGCCTCTTG
501   CTGTTTGCATCCGAATCGTGGTCTCGCTGTTCCTTGGGAGGGTCTCCTCT
551   GAGTGATTGACTACCCACGACGGGGGTCTTTCATTTGGGGGCTCGTCCGG
601   GATTTGGAGACCCCTGCCCAGGGACCACCGACCCACCACCGGGAGGTAAG
651   CTGGCCAGCAACTTATCTGTGTCTGTCCGATTGTCTAGTGTCTATGTTTG
701   ATGTTATGCGCCTGCGTCTGTACTAGTTAGCTAACTAGCTCTGTATCTGG
751   CGGACCCGTGGTGGAACTGACGAGTTCTGAACACCCGGCCGCAACCCTGG
801   GAGACGTCCCAGGGACTTTGGGGGCCGTTTTTGTGGCCCGACCTGAGGAA
851   GGGAGTCGATGTGGAATCCGACCCCGTCAGGATATGTGGTTCTGGTAGGA
901   GACGAGAACCTAAAACAGTTCCCGCCTCCGTCTGAATTTTTGCTTTCGGT
951   TTGGAACCGAAGCCGCGCGTCTTGTCTGCTGCAGCGCTGCAGCATCGTTC
1001  TGTGTTGTCTCTGTCTGACTGTGTTTCTGTATTTGTCTGAAAATTAGGGC
1051  CAGACTGTTACCACTCCCTTAAGTTTGACCTTAGGTCACTGGAAAGATGT
1101  CGAGCGGATCGCTCACAACCAGTCGGTAGATGTCAAGAAGAGACGTTGGG
1151  TTACCTTCTGCTCTGCAGAATGGCCAACCTTTAACGTCGGATGGCCGCGA
1201  GACGGCACCTTTAACCGAGACCTCATCACCCAGGTTAAGATCAAGGTCTT
1251  TTCACCTGGCCCGCATGGACACCCAGACCAGGTCCCCTACATCGTGACCT
1301  GGGAAGCCTTGGCTTTTGACCCCCCTCCCTGGGTCAAGCCCTTTGTACAC
1351  CCTAAGCCTCCGCCTCCTCTTCCTCCATCCGCCCCGTCTCTCCCCCTTGA
1401  ACCTCCTCGTTCGACCCCGCCTCGATCCTCCCTTTATCCAGCCCTCACTC
1451  CTTCTCTAGGCGCCGGAATTCCGATCTGATCAAGAGACAGGATGAGGATC
1501  GTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTT
1551  GGGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGC
1601  TCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTT
1651  TGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAGGACGAGGCAG
1701  CGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTC
1751  GACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCC
1801  GGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCA
1851  TCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGC
1901  CCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGAT
1951  GGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC
2001  TCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGACGGC
2051  GAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGT
2101  GGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGG
2151  CGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAG
2201  CTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGC
2251  TCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCT
2301  GAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGC
2351  CATCACGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGGCTTC
2401  GGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCT
2451  CATGCTGGAGTTCTTCGCCCACCCCGGGCTCGATCCCCTCGCGAGTTGGT
2501  TCAGCTGCTGCCTGAGGCTGGACGACCTCGCGGAGTTCTACCGGCAGTGC
2551  AAATCCGTCGGCATCCAGGAAACCAGCAGCGGCTATCCGCGCATCCATGC
2601  CCCCGAACTGCAGGAGTGGGGAGGCACGATGGCCGCTTTGGTCGAGGCGG
2651  ATCCTAGAACTAGCGAAAATGCAAGAGCAAAGACGAAAACATGCCACACA
2701  TGAGGAATACCGATTCTCTCATTAACATATTCAGGCCAGTTATCTGGGCT
2751  TAAAAGCAGAAGTCCAACCCAGATAACGATCATATACATGGTTCTCTCCA
2801  GAGGTTCATTACTGAACACTCGTCCGAGAATAACGAGTGGATCAGTCCTG
```

Figure 10b

2851 GGTGGTCATTGAAAGGACTGATGCTGAAGTTGAAGCTCCAATACTTTGGC
2901 CACCTGATGCGAAGAACTGACTCATGTGATAAGACCCTGATACTGGGAAA
2951 GATTGAAGGCAGGAGGAGAAGGGATGACAGAGGATGGAAGAGTTGGATGG
3001 AATCACCAACTCGATGGACATGAGTTTGAGCAAGCTTCCAGGAGTTGGTA
3051 ATGGGCAGGGAAGCCTGGCGTGCTGCAGTCCATGGGGTTGCAAAGAGTTG
3101 GACACTACTGAGTGACTGAACTGAACTGATAGTGTAATCCATGGTACAGA
3151 ATATAGGATAAAAAAGAGGAAGAGTTTGCCCTGATTCTGAAGAGTTGTAG
3201 GATATAAAAGTTTAGAATACCTTTAGTTTGGAAGTCTTAAATTATTTACT
3251 TAGGATGGGTACCCACTGCAATATAAGAAATCAGGCTTTAGAGACTGATG
3301 TAGAGAGAATGAGCCCTGGCATACCAGAAGCTAACAGCTATTGGTTATAG
3351 CTGTTATAACCAATATATAACCAATATATTGGTTATATAGCATGAAGCTT
3401 GATGCCAGCAATTTGAAGGAACCATTTAGAACTAGTATCCTAAACTCTAC
3451 ATGTTCCAGGACACTGATCTTAAAGCTCAGGTTCAGAATCTTGTTTTATA
3501 GGCTCTAGGTGTATATTGTGGGGCTTCCCTGGTGGCTCAGATGGTAAAGT
3551 GTCTGCCTGCAATGTGGGTGATCTGGGTTCGATCCCTGGCTTGGGAAGAT
3601 CCCCTGGAGAAGGAAATGGCAACCCACTCTAGTACTCTTACCTGGAAAAT
3651 TCCATGGACAGAGGAGCCTTGTAAGCTACAGTCCATGGGATTGCAAAGAG
3701 TTGAACACAACTGAGCAACTAAGCACAGCACAGTACAGTATACACCTGTG
3751 AGGTGAAGTGAAGTGAAGGTTCAATGCAGGGTCTCCTGCATTGCAGAAAG
3801 ATTCTTTACCATCTGAGCCACCAGGGAAGCCCAAGAATACTGGAGTGGGT
3851 AGCCTATTCCTTCTCCAGGGGATCTTCCCATCCCAGGAATTGAACTGGAG
3901 TCTCCTGCATTTCAGGTGGATTCTTCACCAGCTGAACTACCAGGTGGATA
3951 CTACTCCAATATTAAAGTGCTTAAAGTCCAGTTTTCCCACCTTTCCCAAA
4001 AAGGTTGGGTCACTCTTTTTTAACCTTCTGTGGCCTACTCTGAGGCTGTC
4051 TACAAGCTTATATATTTATGAACACATTTATTGCAAGTTGTTAGTTTTAG
4101 ATTTACAATGTGGTATCTGGCTATTTAGTGGTATTGGTGGTTGGGGATGG
4151 GGAGGCTGATAGCATCTCAGAGGGCAGCTAGATACTGTCATACACACTTT
4201 TCAAGTTCTCCATTTTTGTGAAATAGAAAGTCTCTGGATCTAAGTTATAT
4251 GTGATTCTCAGTCTCTGTGGTCATATTCTATTCTACTCCTGACCACTCAA
4301 CAAGGAACCAAGATATCAAGGGACACTTGTTTTGTTTCATGCCTGGGTTG
4351 AGTGGGCCATGACATATGTTCTGGGCCTTGTTACATGGCTGGATTGGTTG
4401 GACAAGTGCCAGCTCTGATCCTGGGACTGTGGCATGTGATGACATACACC
4451 CCCTCTCCACATTCTGCATGTCTCTAGGGGGGAAGGGGGAAGCTCGGTAT
4501 AGAACCTTTATTGTATTTTCTGATTGCCTCACTTCTTATATTGCCCCCAT
4551 GCCCTTCTTTGTTCCTCAAGTAACCAGAGACAGTGCTTCCCAGAACCAAC
4601 CCTACAAGAAACAAAGGGCTAAACAAAGCCAAATGGGAAGCAGGATCATG
4651 GTTTGAACTCTTTCTGGCCAGAGAACAATACCTGCTATGGACTAGATACT
4701 GGGAGAGGGAAAGGAAAAGTAGGGTGAATTATGGAAGGAAGCTGGCAGGC
4751 TCAGCGTTTCTGTCTTGGCATGACCAGTCTCTCTTCATTCTCTTCCTAGA
4801 TGTAGGGCTTGGTACCAGAGCCCCTGAGGCTTTCTGCATGAATATAAATA
4851 TATGAAACTGAGTGATGCTTCCATTTCAGGTTCTTGGGGGCGCCGAATTC
4901 GAGCTCGGTACCCGGGGATCTCGACGGATCCGATTACTTACTGGCAGGTG
4951 CTGGGGGCTTCCGAGACAATCGCGAACATCTACACCACACAACACCGCCT
5001 CGACCAGGGTGAGATATCGGCCGGGGACGCGGCGGTGGTAATTACAAGCG
5051 AGATCCGATTACTTACTGGCAGGTGCTGGGGGCTTCCGAGACAATCGCGA
5101 ACATCTACACCACACAACACCGCCTCGACCAGGGTGAGATATCGGCCGGG
5151 GACGCGGCGGTGGTAATTACAAGCGAGATCCCCGGGAATTCAGGACCTCA
5201 CCATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGT
5251 GTCCACTCCGAGGTCCAACTGGTGGAGAGCGGTGGAGGTGTTGTGCAACC
5301 TGGCCGGTCCCTGCGCCTGTCCTGCTCCGCATCTGGCTTCGATTTCACCA
5351 CATATTGGATGAGTTGGGTGAGACAGGCACCTGGAAAAGGTCTTGAGTGG
5401 ATTGGAGAAATTCATCCAGATAGCAGTACGATTAACTATGCGCCGTCTCT
5451 AAAGGATAGATTTACAATATCGCGAGACAACGCCAAGAACACATTGTTCC
5501 TGCAAATGGACAGCCTGAGACCCGAAGACACCGGGGTCTATTTTTGTGCA
5551 AGCCTTTACTTCGGCTTCCCCTGGTTTGCTTATTGGGGCCAAGGGACCCC
5601 GGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGG
5651 CACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTG
5701 GTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGC
5751 CCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGAC
5801 TCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
5851 CAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGA
5901 CAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGT

Figure 10c

```
5951  GCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCA
6001  AAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGT
6051  GGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACG
6101  TGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG
6151  TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGA
6201  CTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCC
6251  CAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAA
6301  CCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCA
6351  GGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCG
6401  TGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT
6451  CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGT
6501  GGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGC
6551  ACGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCC
6601  GGGAAATGAAAGCCGAATTCGCCCCTCTCCCTCCCCCCCCCCTAACGTTA
6651  CTGGCCGAAGCCGCTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTA
6701  TTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGG
6751  CCCTGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAG
6801  GAATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCT
6851  TCTTGAAGACAAACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCC
6901  CCCACCTGGCGACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATA
6951  CACCTGCAAAGGCGGCACAACCCCAGTGCCACGTTGTGAGTTGGATAGTT
7001  GTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAA
7051  GGATGCCCAGAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGT
7101  GCACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAAACGTCTAGGCCCC
7151  CCGAACCACGGGGACGTGGTTTTCCTTTGAAAAACACGATGATAATATGG
7201  CCTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAG
7251  GCCGACATCCAGCTGACCCAGAGCCCAAGCAGCCTGAGCGCCAGCGTGGG
7301  TGACAGAGTGACCATCACCTGTAAGGCCAGTCAGGATGTGGGTACTTCTG
7351  TAGCCTGGTACCAGCAGAAGCCAGGTAAGGCTCCAAAGCTGCTGATCTAC
7401  TGGACATCCACCCGGCACACTGGTGTGCCAAGCAGATTCAGCGGTAGCGG
7451  TAGCGGTACCGACTTCACCTTCACCATCAGCAGCCTCCAGCCAGAGGACA
7501  TCGCCACCTACTACTGCCAGCAATATAGCCTCTATCGGTCGTTCGGCCAA
7551  GGGACCAAGGTGGAAATCAAACGAACTGTGGCTGCACCATCTGTCTTCAT
7601  CTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT
7651  GCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTG
7701  GATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA
7751  CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAG
7801  CAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGC
7851  CTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAGATC
7901  CCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATAATCAACCTCTGG
7951  ATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCT
8001  TTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGC
8051  TTCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTGCTGT
8101  CTCTTTATGAGGAGTTGTGGCCCGTTGTCAGGCAACGTGGCGTGGTGTGC
8151  ACTGTGTTTGCTGACGCAACCCCCACTGGTTGGGGCATTGCCACCACCTG
8201  TCAGCTCCTTTCCGGGACTTTCGCTTTCCCCCTCCCTATTGCCACGGCGG
8251  AACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTG
8301  GGCACTGACAATTCCGTGGTGTTGTCGGGGAAATCATCGTCCTTTCCTTG
8351  GCTGCTCGCCTGTGTTGCCACCTGGATTCTGCGCGGGACGTCCTTCTGCT
8401  ACGTCCCTTCGGCCCTCAATCCAGCGGACCTTCCTTCCCGCGGCCTGCTG
8451  CCGGCTCTGCGGCCTCTTCCGCGTCTTCGCCTTCGCCCTCAGACGAGTCG
8501  GATCTCCCTTTGGGCCGCCTCCCCGCCTGATCGATACCGTCAACATCGAT
8551  AAAATAAAAGATTTTATTTAGTCTCCAGAAAAAGGGGGGAATGAAAGACC
8601  CCACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGCAAGGCA
8651  TGGAAAAATACATAACTGAGAATAGAGAAGTTCAGATCAAGGTCAGGAAC
8701  AGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTT
8751  CCTGCCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGGCCA
8801  AACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAAC
8851  AGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGAGAACCATC
8901  AGATGTTTCCAGGGTGCCCCAAGGACCTGAAATGACCCTGTGCCTTATTT
8951  GAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCTTCTGCTCC
9001  CCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGGGCGCCAGTCCTC
```

Figure 10d

```
9051  CGATTGACTGAGTCGCCCGGGTACCCGTGTATCCAATAAACCCTCTTGCA
9101  GTTGCATCCGACTTGTGGTCTCGCTGTTCCTTGGGAGGGTCTCCTCTGAG
9151  TGATTGACTACCCGTCAGCGGGGGTCTTTCATT
```

1 - 658	MoMuSV 5' LTR
659 - 1468	Extended packaging region
1512 - 2306	Neomycin resistance gene
2661 - 4896	Bovine/human alpha-lactalbumin 5' flanking region
5084 - 5327	Double mutated PPE sequence
6207 - 6209	MN14 antibody heavy chain gene signal peptide start codon
6611-6613	MN14 antibody heavy chain stop codon
6625 - 7200	EMCV IRES
7201 - 7203	Bovine alpha-lactalbumin signal peptide start codon
7258 - 7260	First codon of mature MN14 antibody light chain gene
7897 - 7899	MN14 antibody light gene stop codon
7938 - 8529	WPRE sequence
8600 - 9138	Moloney murine leukemia virus 3' LTR

Figure 11a
SEQ ID NO:8
Alpha-Lactalbumin Bot Vector

```
1     GATCAGTCCTGGGTGGTCATTGAAAGGACTGATGCTGAAGTTGAAGCTCC
51    AATACTTTGGCCACCTGATGCGAAGAACTGACTCATGTGATAAGACCCTG
101   ATACTGGGAAAGATTGAAGGCAGGAGGAGAAGGGATGACAGAGGATGGAA
151   GAGTTGGATGGAATCACCAACTCGATGGACATGAGTTTGAGCAAGCTTCC
201   AGGAGTTGGTAATGGGCAGGGAAGCCTGGCGTGCTGCAGTCCATGGGGTT
251   GCAAAGAGTTGGACACTACTGAGTGACTGAACTGAACTGATAGTGTAATC
301   CATGGTACAGAATATAGGATAAAAAAGAGGAAGAGTTTGCCCTGATTCTG
351   AAGAGTTGTAGGATATAAAAGTTTAGAATACCTTTAGTTTGGAAGTCTTA
401   AATTATTTACTTAGGATGGGTACCCACTGCAATATAAGAAATCAGGCTTT
451   AGAGACTGATGTAGAGAGAATGAGCCCTGGCATACCAGAAGCTAACAGCT
501   ATTGGTTATAGCTGTTATAACCAATATATAACCAATATATTGGTTATATA
551   GCATGAAGCTTGATGCCAGCAATTTGAAGGAACCATTTAGAACTAGTATC
601   CTAAACTCTACATGTTCCAGGACACTGATCTTAAAGCTCAGGTTCAGAAT
651   CTTGTTTTATAGGCTCTAGGTGTATATTGTGGGGCTTCCCTGGTGGCTCA
701   GATGGTAAAGTGTCTGCCTGCAATGTGGGTGATCTGGGTTCGATCCCTGG
751   CTTGGGAAGATCCCCTGGAGAAGGAAATGGCAACCCACTCTAGTACTCTT
801   ACCTGGAAAATTCCATGGACAGAGGAGCCTTGTAAGCTACAGTCCATGGG
851   ATTGCAAAGAGTTGAACACAACTGAGCAACTAAGCACAGCACAGTACAGT
901   ATACACCTGTGAGGTGAAGTGAAGTGAAGGTTCAATGCAGGGTCTCCTGC
951   ATTGCAGAAAGATTCTTTACCATCTGAGCCACCAGGGAAGCCCAAGAATA
1001  CTGGAGTGGGTAGCCTATTCCTTCTCCAGGGGATCTTCCCATCCCAGGAA
1051  TTGAACTGGAGTCTCCTGCATTTCAGGTGGATTCTTCACCAGCTGAACTA
1101  CCAGGTGGATACTACTCCAATATTAAAGTGCTTAAAGTCCAGTTTTCCCA
1151  CCTTTCCCAAAAAGGTTGGGTCACTCTTTTTTAACCTTCTGTGGCCTACT
1201  CTGAGGCTGTCTACAAGCTTATATATTTATGAACACATTTATTGCAAGTT
1251  GTTAGTTTTAGATTTACAATGTGGTATCTGGCTATTTAGTGGTATTGGTG
1301  GTTGGGGATGGGGAGGCTGATAGCATCTCAGAGGGCAGCTAGATACTGTC
1351  ATACACACTTTTCAAGTTCTCCATTTTTGTGAAATAGAAAGTCTCTGGAT
1401  CTAAGTTATATGTGATTCTCAGTCTCTGTGGTCATATTCTATTCTACTCC
1451  TGACCACTCAACAAGGAACCAAGATATCAAGGGACACTTGTTTTGTTTCA
1501  TGCCTGGGTTGAGTGGGCCATGACATATGTTCTGGGCCTTGTTACATGGC
1551  TGGATTGGTTGGACAAGTGCCAGCTCTGATCCTGGGACTGTGGCATGTGA
1601  TGACATACACCCCCTCTCCACATTCTGCATGTCTCTAGGGGGGAAGGGGG
1651  AAGCTCGGTATAGAACCTTTATTGTATTTTCTGATTGCCTCACTTCTTAT
1701  ATTGCCCCCATGCCCTTCTTTGTTCCTCAAGTAACCAGAGACAGTGCTTC
1751  CCAGAACCAACCCTACAAGAAACAAAGGGCTAAACAAAGCCAAATGGGAA
1801  GCAGGATCATGGTTTGAACTCTTTCTGGCCAGAGAACAATACCTGCTATG
1851  GACTAGATACTGGGAGAGGGAAAGGAAAAGTAGGGTGAATTATGGAAGGA
1901  AGCTGGCAGGCTCAGCGTTTCTGTCTTGGCATGACCAGTCTCTCTTCATT
1951  CTCTTCCTAGATGTAGGGCTTGGTACCAGAGCCCCTGAGGCTTTCTGCAT
2001  GAATATAAATATATGAAACTGAGTGATGCTTCCATTTCAGGTTCTTGGGG
2051  GCGCCGAATTCGAGCTCGGTACCCGGGGATCTCGACGGATCCGATTACTT
2101  ACTGGCAGGTGCTGGGGGCTTCCGAGACAATCGCGAACATCTACACCACA
2151  CAACACCGCCTCGACCAGGGTGAGATATCGGCCGGGGACGCGGCGGTGGT
2201  AATTACAAGCGAGATCCGATTACTTACTGGCAGGTGCTGGGGGCTTCCGA
2251  GACAATCGCGAACATCTACACCACACAACACCGCCTCGACCAGGGTGAGA
2301  TATCGGCCGGGGACGCGGCGGTGGTAATTACAAGCGAGATCTCGAGAAGC
2351  TTGTTGGGAATTCAGGCCATCGATCCCGCCGCCACCATGGAATGGAGCTG
2401  GGTCTTTCTCTTCTTCCTGTCAGTAACTACAGGTGTCCACTCCGACATCC
2451  AGATGACCCAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAGAAACTGTC
2501  ACTATCACATGTCGAGCAAGTGGGAATATTCACAATTATTTAGCATGGTA
2551  TCAGCAGAAACAGGGAAAATCTCCTCAGCTCCTGGTCTATAATGCAAAAA
2601  CCTTAGCAGATGGTGTGCCATCAAGGTTCAGTGGCAGTGGATCAGGAACA
2651  CAATATTCTCTCAAGATCAACAGCCTGCAGCCTGAAGATTTTGGGAGTTA
2701  TTACTGTCAACATTTTTGGAGTACTCCGTGGACGTTCGGTGGAGGCACCA
2751  AGCTGGAAATCAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCCA
2801  CCATCCAGTGAGCAGTTAACATCTGGAGGTGCCTCAGTCGTGTGCTTCTT
```

Figure 11b

```
2851   GAACAACTTCTACCCCAAAGACATCAATGTCAAGTGGAAGATTGATGGCA
2901   GTGAACGACAAAATGGCGTCCTGAACAGTTGGACTGATCAGGACAGCAAA
2951   GACAGCACCTACAGCATGAGCAGCACCCTCACATTGACCAAGGACGAGTA
3001   TGAACGACATAACAGCTATACCTGTGAGGCCACTCACAAGACATCAACTT
3051   CACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTTGAAAGCATCGATTT
3101   CCCCTGAATTCGCCCCTCTCCCTCCCCCCCCCCTAACGTTACTGGCCGAA
3151   GCCGCTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTATTTTCCACC
3201   ATATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCTGTCTT
3251   CTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGAATGCAAG
3301   GTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGA
3351   CAAACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCCCCACCTGG
3401   CGACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAA
3451   AGGCGGCACAACCCCAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGA
3501   GTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCCA
3551   GAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTGCACATGCT
3601   TTACATGTGTTTAGTCGAGGTTAAAAAAACGTCTAGGCCCCCCGAACCAC
3651   GGGGACGTGGTTTTCCTTTGAAAAACACGATGATAATATGGCCTCCTTTG
3701   TCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCCGAGGTT
3751   CAGCTTCAGCAGTCTGGGGCAGAGCTTGTGAAGCCAGGGGCCTCAGTCAA
3801   GTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAGACACCTTTATGCACT
3851   GGGTGAAGCAGAGGCCTGAACAGGGCCTGGAGTGGATTGGAAGGATTGAT
3901   CCTGCGAATGGGAATACTGAATATGACCCGAAGTTCCAGGGCAAGGCCAC
3951   TATAACAGCAGACACATCCTCCAACACAGTCAACCTGCAGCTCAGCAGCC
4001   TGACATCTGAGGACACTGCCGTCTATTACTGTGCTAGTGGAGGGGAACTG
4051   GGGTTTCCTTACTGGGGCCAAGGGACTCTGGTCACTGTCTCTGCAGCCAA
4101   AACGACACCCCCATCTGTCTATCCACTGGCCCCTGGATCTGCTGCCCAAA
4151   CTAACTCCATGGTGACCCTGGGATGCCTGGTCAAGGGCTATTTCCCTGAG
4201   CCAGTGACAGTGACCTGGAACTCTGGATCCCTGTCCAGCGGTGTGCACAC
4251   CTTCCCAGCTGTCCTGCAGTTTGACCTCTACACTCTGAGCAGCTCAGTGA
4301   CTGTCCCCTCCAGCACCTGGCCCAGCGAGACCGTCACCTGCAACGTTGCC
4351   CACCCGGCCAGCAGCACCAAGGTGGACAAGAAAATTGTGCCCAGGGATTG
4401   TACTAGTGGAGGTGGAGGTAGCCACCATCACCATCACCATTAATCTAGAG
4451   TTAAGCGGCCGTCGAGATCTCGACATCGATAATCAACCTCTGGATTACAA
4501   AATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGC
4551   TATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGT
4601   ATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTGCTGTCTCTTTA
4651   TGAGGAGTTGTGGCCCGTTGTCAGGCAACGTGGCGTGGTGTGCACTGTGT
4701   TTGCTGACGCAACCCCCACTGGTTGGGGCATTGCCACCACCTGTCAGCTC
4751   CTTTCCGGGACTTTCGCTTTCCCCCTCCCTATTGCCACGGCGGAACTCAT
4801   CGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTG
4851   ACAATTCCGTGGTGTTGTCGGGGAAATCATCGTCCTTTCCTTGGCTGCTC
4901   GCCTGTGTTGCCACCTGGATTCTGCGCGGGACGTCCTTCTGCTACGTCCC
4951   TTCGGCCCTCAATCCAGCGGACCTTCCTTCCCGCGGCCTGCTGCCGGCTC
5001   TGCGGCCTCTTCCGCGTCTTCGCCTTCGCCCTCAGACGAGTCGGATCTCC
5051   CTTTGGGCCGCCTCCCCGCCTGATCGATAAAATAAAAGATTTTATTTAGT
5101   CTCCAGAAAAAGGGGGGAATGAAAGACCCCACCTGTAGGTTTGGCAAGCT
5151   AGCTTAAGTAACGCCATTTTGCAAGGCATGGAAAAATACATAACTGAGAA
5201   TAGAGAAGTTCAGATCAAGGTCAGGAACAGATGGAACAGCTGAATATGGG
5251   CCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAG
5301   AACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCA
5351   GTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCC
5401   AGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAA
5451   GGACCTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTCGCTT
5501   CTCGCTTCTGTTCGCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCCA
5551   CAACCCCTCACTCGGGGCGCCAGTCCTCCGATTGACTGAGTCGCCCGGGT
5601   ACCCGTGTATCCAATAAACCCTCTTGCAGTTGCATCCGACTTGTGGTCTC
```

Figure 11c

5651 GCTGTTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGG
5701 GGTCTTTCATT

1 - 2053	Bovine/human alpha-lactalbumin 5' flanking region
2093 - 2336	Double mtated PPE sequence
2387 - 2443	cc49 signal peptide coding region
2444 - 3088	Bot antibody light chain Fab coding region
3112 - 3686	EMCV IRES
3687 - 3745	Bovine alpha-lactalbumin signal peptide coding region
3746 - 4443	Bot antibody heavy chain Fab coding region
4481 - 5072	WPRE sequence
5118 - 5711	Moloney murine leukemia virus 3' LTR

Figure 12a
SEQ ID NO:9
LSNRL Vector

```
1     TTTGAAAGACCCCACCCGTAGGTGGCAAGCTAGCTTAAGTAACGCCACTT
51    TGCAAGGCATGGAAAAATACATAACTGAGAATAGAAAAGTTCAGATCAAG
101   GTCAGGAACAAAGAAACAGCTGAATACCAAACAGGATATCTGTGGTAAGC
151   GGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGAGACAGCTGAGTGATG
201   GGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCGGGGCCA
251   AGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGTGAA
301   TCATCAGATGTTTCCAGGGTGCCCCAAGGACCTGAAAATGACCCTGTACC
351   TTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCTTC
401   CGCTCTCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGCGCGCCA
451   GTCTTCCGATAGACTGCGTCGCCCGGGTACCCGTATTCCCAATAAAGCCT
501   CTTGCTGTTTGCATCCGAATCGTGGTCTCGCTGTTCCTTGGGAGGGTCTC
551   CTCTGAGTGATTGACTACCCACGACGGGGGTCTTTCATTTGGGGGCTCGT
601   CCGGGATTTGGAGACCCCTGCCCAGGGACCACCGACCCACCACCGGGAGG
651   TAAGCTGGCCAGCAACTTATCTGTGTCTGTCCGATTGTCTAGTGTCTATG
701   TTTGATGTTATGCGCCTGCGTCTGTACTAGTTAGCTAACTAGCTCTGTAT
751   CTGGCGGACCCGTGGTGGAACTGACGAGTTCTGAACACCCGGCCGCAACC
801   CTGGGAGACGTCCCAGGGACTTTGGGGGCCGTTTTTGTGGCCCGACCTGA
851   GGAAGGGAGTCGATGTGGAATCCGACCCCGTCAGGATATGTGGTTCTGGT
901   AGGAGACGAGAACCTAAAACAGTTCCCGCCTCCGTCTGAATTTTTGCTTT
951   CGGTTTGGAACCGAAGCCGCGCGTCTTGTCTGCTGCAGCCAAGCTTGGGC
1001  TGCAGGTCGAGGACTGGGGACCCTGCACCGAACATGGAGAACACAACATC
1051  AGGATTCCTAGGACCCCTGCTCGTGTTACAGGCGGGGTTTTTCTTGTTGA
1101  CAAGAATCCTCACAATACCACAGAGTCTAGACTCGTGGTGGACTTCTCTC
1151  AATTTTCTAGGGGGAGCACCCACGTGTCCTGGCCAAAATTCGCAGTCCCC
1201  AACCTCCAATCACTCACCAACCTCTTGTCCTCCAATTTGTCCTGGCTATC
1251  GCTGGATGTGTCTGCGGCGTTTTATCATATTCCTCTTCATCCTGCTGCTA
1301  TGCCTCATCTTCTTGTTGGTTCTTCTGGACTACCAAGGTATGTTGCCCGT
1351  TTGTCCTCTACTTCCAGGAACATCAACTACCAGCACGGGACCATGCAAGA
1401  CCTGCACGATTCCTGCTCAAGGAACCTCTATGTTTCCCTCTTGTTGCTGT
1451  ACAAAACCTTCGGACGGAAACTGCACTTGTATTCCCATCCCATCATCCTG
1501  GGCTTTCGCAAGATTCCTATGGGAGTGGGCCTCAGTCCGTTTCTCCTGGC
1551  TCAGTTTACTAGTGCCATTTGTTCAGTGGTTCGTAGGGCTTTCCCCCACT
1601  GTTTGGCTTTCAGTTATATGGATGATGTGGTATTGGGGGCCAAGTCTGTA
1651  CAACATCTTGAGTCCCTTTTTACCTCTATTACCAATTTTCTTTTGTCTTT
1701  GGGTATACATTTAAACCCTAATAAAACCAAACGTTGGGGCTACTCCCTTA
1751  ACTTCATGGGATATGTAATTGGATGTTGGGGTACTTTACCGCAAGAACAT
1801  ATTGTACTAAAAATCAAGCAATGTTTTCGAAAACTGCCTGTAAATAGACC
1851  TATTGATTGGAAAGTATGTCAGAGACTTGTGGGTCTTTTGGGCTTTGCTG
1901  CCCCTTTTACACAATGTGGCTATCCTGCCTTAATGCCTTTATATGCATGT
1951  ATACAATCTAAGCAGGCTTTCACTTTCTCGCCAACTTACAAGGCCTTTCT
2001  GTGTAAACAATATCTGAACCTTTACCCCGTTGCCCGGCAACGGTCAGGTC
2051  TCTGCCAAGTGTTTGCTGACGCAACCCCCACTGGATGGGGCTTGGCTATC
2101  GGCCATAGCCGCATGCGCGGACCTTTGTGGCTCCTCTGCCGATCCATACT
2151  GCGGAACTCCTAGCAGCTTGTTTTGCTCGCAGGCGGTCTGGAGCGAAACT
2201  TATCGGCACCGACAACTCTGTTGTCCTCTCTCGGAAATACACCTCCTTTC
2251  CATGGCTGCTAGGGTGTGCTGCCAACTGGATCCCCTCAGGATATAGTAGT
2301  TTCGCTTTTGCATAGGGAGGGGGAAATGTAGTCTTATGCAATACACTTGT
2351  AGTCTTGCAACATGGTAACGATGAGTTAGCAACATGCCTTACAAGGAGAG
2401  AAAAAGCACCGTGCATGCCGATTGGTGGAAGTAAGGTGGTACGATCGTGC
2451  CTTATTAGGAAGGCAACAGACAGGTCTGACATGGATTGGACGAACCACTG
2501  AATTCCGCATTGCAGAGATAATTGTATTTAAGTGCCTAGCTCGATACAGC
2551  AAACGCCATTTTTGACCATTCACCACATTGGTGTGCACCTTCCAAAGCTT
2601  CACGCTGCCGCAAGCACTCAGGGCGCAAGGGCTGCTAAAGGAAGCGGAAC
2651  ACGTAGAAAGCCAGTCCGCAGAAACGGTGCTGACCCCGGATGAATGTCAG
2701  CTACTGGGCTATCTGGACAAGGGAAAACGCAAGCGCAAAGAGAAAGCAGG
2751  TAGCTTGCAGTGGGCTTACATGGCGATAGCTAGACTGGGCGGTTTTATGG
2801  ACAGCAAGCGAACCGGAATTGCCAGCTGGGGCGCCCTCTGGTAAGGTTGG
```

Figure 12b

```
2851   GAAGCCCTGCAAAGTAAACTGGATGGCTTTCTTGCCGCCAAGGATCTGAT
2901   GGCGCAGGGGATCAAGATCTGATCAAGAGACAGGATGAGGATCGTTTCGC
2951   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGA
3001   GAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATG
3051   CCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAG
3101   ACCGACCTGTCCGGTGCCCTGAATGAACTGCAGGACGAGGCAGCGCGGCT
3151   ATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTG
3201   TCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG
3251   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGC
3301   TGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCG
3351   ACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCC
3401   GGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCC
3451   AGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGACGGCGAGGATC
3501   TCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT
3551   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCG
3601   CTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCG
3651   GCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGAT
3701   TCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGG
3751   ACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATCACG
3801   AGATTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGGCTTCGGAATCG
3851   TTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTG
3901   GAGTTCTTCGCCCACCCCAACCCTGGCCCTATTATTGGGTGGACTAACCA
3951   TGGGGGGAATTGCCGCTGGAATAGGAACAGGGACTACTGCTCTAATGGCC
4001   ACTCAGCAATTCCAGCAGCTCCAAGCCGCAGTACAGGATGATCTCAGGGA
4051   GGTTGAAAAATCAATCTCTAACCTAGAAAAGTCTCTCACTTCCCTGTCTG
4101   AAGTTGTCCTACAGAATCGAAGGGGCCTAGACTTGTTATTTCTAAAAGAA
4151   GGAGGGCTGTGTGCTGCTCTAAAAGAAGAATGTTGCTTCTATGCGGACCA
4201   CACAGGACTAGTGAGAGACAGCATGGCCAAATTGAGAGAGAGGCTTAATC
4251   AGAGACAGAAACTGTTTGAGTCAACTCAAGGATGGTTTGAGGGACTGTTT
4301   AACAGATCCCCTTGGTTTACCACCTTGATATCTACCATTATGGGACCCCT
4351   CATTGTACTCCTAATGATTTTGCTCTTCGGACCCTGCATTCTTAATCGAT
4401   TAGTCCAATTTGTTAAAGACAGGATATCAGTGGTCCAGGCTCTAGTTTTG
4451   ACTCAACAATATCACCAGCTGAAGCCTATAGAGTACGAGCCATAGATAAA
4501   ATAAAAGATTTTATTTAGTCTCCAGAAAAAGGGGGGAATGAAAGACCCCA
4551   CCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGCAAGGCATGG
4601   AAAAATACATAACTGAGAATAGAGAAGTTCAGATCAAGGTCAGGAACAGA
4651   TGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCT
4701   GCCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGGCCAAAC
4751   AGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGA
4801   TGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGAGAACCATCAGA
4851   TGTTTCCAGGGTGCCCCAAGGACCTGAAATGACCCTGTGCCTTATTTGAA
4901   CTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCTTCTGCTCCCCG
4951   AGCTCAATAAAAGAGCCCACAACCCCTCACTCGGGGCGCCAGTCCTCCGA
5001   TTGACTGAGTCGCCCGGGTACCCGTGTATCCAATAAACCCTCTTGCAGTT
5051   GCATCCGACTTGTGGTCTCGCTGTTCCTTGGGAGGGTCTCCTCTGAGTGA
5101   TTGACTACCCGTCAGCGGGGGTCTTTCATT
```

1 - 589	MoMuSV 5' LTR
659 - 897	Retroviral packaging region
1034 - 1714	Hepatitis B surface antigen
2279 - 2595	RSV promoter
2951 - 3745	Neomycin phosphotransferase gene
4537 - 5130	MoMuLV 3' LTR

Figure 13a
SEQ ID NO:10
Alpha-Lactalbumin cc49IL2 Vector

```
1     GATCAGTCCTGGGTGGTCATTGAAAGGACTGATGCTGAAGTTGAAGCTCC
51    AATACTTTGGCCACCTGATGCGAAGAACTGACTCATGTGATAAGACCCTG
101   ATACTGGGAAAGATTGAAGGCAGGAGGAGAAGGGATGACAGAGGATGGAA
151   GAGTTGGATGGAATCACCAACTCGATGGACATGAGTTTGAGCAAGCTTCC
201   AGGAGTTGGTAATGGGCAGGGAAGCCTGGCGTGCTGCAGTCCATGGGGTT
251   GCAAAGAGTTGGACACTACTGAGTGACTGAACTGAACTGATAGTGTAATC
301   CATGGTACAGAATATAGGATAAAAAAGAGGAAGAGTTTGCCCTGATTCTG
351   AAGAGTTGTAGGATATAAAAGTTTAGAATACCTTTAGTTTGGAAGTCTTA
401   AATTATTTACTTAGGATGGGTACCCACTGCAATATAAGAAATCAGGCTTT
451   AGAGACTGATGTAGAGAGAATGAGCCCTGGCATACCAGAAGCTAACAGCT
501   ATTGGTTATAGCTGTTATAACCAATATATAACCAATATATTGGTTATATA
551   GCATGAAGCTTGATGCCAGCAATTTGAAGGAACCATTTAGAACTAGTATC
601   CTAAACTCTACATGTTCCAGGACACTGATCTTAAAGCTCAGGTTCAGAAT
651   CTTGTTTTATAGGCTCTAGGTGTATATTGTGGGGCTTCCCTGGTGGCTCA
701   GATGGTAAAGTGTCTGCCTGCAATGTGGGTGATCTGGGTTCGATCCCTGG
751   CTTGGGAAGATCCCCTGGAGAAGGAAATGGCAACCCACTCTAGTACTCTT
801   ACCTGGAAAATTCCATGGACAGAGGAGCCTTGTAAGCTACAGTCCATGGG
851   ATTGCAAAGAGTTGAACACAACTGAGCAACTAAGCACAGCACAGTACAGT
901   ATACACCTGTGAGGTGAAGTGAAGTGAAGGTTCAATGCAGGGTCTCCTGC
951   ATTGCAGAAAGATTCTTTACCATCTGAGCCACCAGGGAAGCCCAAGAATA
1001  CTGGAGTGGGTAGCCTATTCCTTCTCCAGGGGATCTTCCCATCCCAGGAA
1051  TTGAACTGGAGTCTCCTGCATTTCAGGTGGATTCTTCACCAGCTGAACTA
1101  CCAGGTGGATACTACTCCAATATTAAAGTGCTTAAAGTCCAGTTTTCCCA
1151  CCTTTCCCAAAAAGGTTGGGTCACTCTTTTTTAACCTTCTGTGGCCTACT
1201  CTGAGGCTGTCTACAAGCTTATATATTTATGAACACATTTATTGCAAGTT
1251  GTTAGTTTTAGATTTACAATGTGGTATCTGGCTATTTAGTGGTATTGGTG
1301  GTTGGGGATGGGGAGGCTGATAGCATCTCAGAGGGCAGCTAGATACTGTC
1351  ATACACACTTTTCAAGTTCTCCATTTTTGTGAAATAGAAAGTCTCTGGAT
1401  CTAAGTTATATGTGATTCTCAGTCTCTGTGGTCATATTCTATTCTACTCC
1451  TGACCACTCAACAAGGAACCAAGATATCAAGGGACACTTGTTTTGTTTCA
1501  TGCCTGGGTTGAGTGGGCCATGACATATGTTCTGGGCCTTGTTACATGGC
1551  TGGATTGGTTGGACAAGTGCCAGCTCTGATCCTGGGACTGTGGCATGTGA
1601  TGACATACACCCCCTCTCCACATTCTGCATGTCTCTAGGGGGGAAGGGGG
1651  AAGCTCGGTATAGAACCTTTATTGTATTTTCTGATTGCCTCACTTCTTAT
1701  ATTGCCCCCATGCCCTTCTTTGTTCCTCAAGTAACCAGAGACAGTGCTTC
1751  CCAGAACCAACCCTACAAGAAACAAAGGGCTAAACAAAGCCAAATGGGAA
1801  GCAGGATCATGGTTTGAACTCTTTCTGGCCAGAGAACAATACCTGCTATG
1851  GACTAGATACTGGGAGAGGGAAAGGAAAAGTAGGGTGAATTATGGAAGGA
1901  AGCTGGCAGGCTCAGCGTTTCTGTCTTGGCATGACCAGTCTCTCTTCATT
1951  CTCTTCCTAGATGTAGGGCTTGGTACCAGAGCCCCTGAGGCTTTCTGCAT
2001  GAATATAAATATATGAAACTGAGTGATGCTTCCATTTCAGGTTCTTGGGG
2051  GCGCCGAATTCGAGCTCGGTACCCGGGGATCTCGAGAAGCTTTAACCATG
2101  GAATGGAGCTGGGTCTTTCTCTTCTTCCTGTCAGTAACTACAGGTGTCCA
2151  CTCCCAGGTTCAGTTGCAGCAGTCTGACGCTGAGTTGGTGAAACCTGGGG
2201  CTTCAGTGAAGATTTCCTGCAAGGCTTCTGGCTACACCTTCACTGACCAT
2251  GCAATTCACTGGGTGAAACAGAACCCTGAACAGGGCCTGGAATGGATTGG
2301  ATATTTTTCTCCCGGAAATGATGATTTTAAATACAATGAGAGGTTCAAGG
2351  GCAAGGCCACACTGACTGCAGACAAATCCTCCAGCACTGCCTACGTGCAG
2401  CTCAACAGCCTGACATCTGAGGATTCTGCAGTGTATTTCTGTACAAGATC
2451  CCTGAATATGGCCTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAG
2501  GAGGCGGAGGCAGCGGAGGCGGTGGCTCGGGAGGCGGAGGCTCGGACATT
2551  GTGATGTCACAGTCTCCATCCTCCCTACCTGTGTCAGTTGGCGAGAAGGT
2601  TACTTTGAGCTGCAAGTCCAGTCAGAGCCTTTTATATAGTGGTAATCAAA
2651  AGAACTACTTGGCCTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTG
2701  CTGATTTACTGGGCATCCGCTAGGGAATCTGGGGTCCCTGATCGCTTCAC
2751  AGGCAGTGGATCTGGGACAGATTTCACTCTCTCCATCAGCAGTGTGAAGA
2801  CTGAAGACCTGGCAGTTTATTACTGTCAGCAGTATTATAGCTATCCCCTC
```

Figure 13b

```
2851  ACGTTCGGTGCTGGGACCAAGCTGGTGCTGAAACGGGCCGCCGAGCCCAA
2901  ATCTCCTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC
2951  TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC
3001  ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCA
3051  CGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGC
3101  ATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGT
3151  GTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGA
3201  GTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA
3251  CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG
3301  CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCT
3351  GGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATG
3401  GGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGAC
3451  GGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCA
3501  GCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC
3551  ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGGAGGCGGATCA
3601  GGAGGTGGCGCACCTACTTCAAGTTCTACAAAGAAAACACAGCTACAACT
3651  GGAGCATTTACTGCTGGATTTACAGATGATTTTGAATGGAATTAATAATT
3701  ACAAGAATCCCAAACTCACCAGGATGCTCACATTTAAGTTTTACATGCCC
3751  AAGAAGGCCACAGAACTGAAACATCTTCAGTGTCTAGAAGAAGAACTCAA
3801  ACCTCTGGAGGAAGTGCTAAATTTAGCTCAAAGCAAAAACTTTCACTTAA
3851  GACCCAGGGACTTAATCAGCAATATCAACGTAATAGTTCTGGAACTAAAG
3901  GGATCTGAAACAACATTCATGTGTGAATATGCTGATGAGACAGCAACCAT
3951  TGTAGAATTTCTGAACAGATGGATTACCTTTTGTCAAAGCATCATCTCAA
4001  CACTAACTTGAAGCTTGTTAACATCGATAAAATAAAAGATTTTATTTAGT
4051  CTCCAGAAAAAGGGGGGAATGAAAGACCCCACCTGTAGGTTTGGCAAGCT
4101  AGCTTAAGTAACGCCATTTTGCAAGGCATGGAAAAATACATAACTGAGAA
4151  TAGAGAAGTTCAGATCAAGGTCAGGAACAGATGGAACAGCTGAATATGGG
4201  CCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAG
4251  AACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCA
4301  GTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCC
4351  AGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAA
4401  GGACCTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTCGCTT
4451  CTCGCTTCTGTTCGCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCCA
4501  CAACCCCTCACTCGGGGCGCCAGTCCTCCGATTGACTGAGTCGCCCGGGT
4551  ACCCGTGTATCCAATAAACCCTCTTGCAGTTGCATCCGACTTGTGGTCTC
4601  GCTGTTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGG
4651  GGTCTTTCATT
```

1 - 2055	Bovine/human alpha-lactalbumin 5' flanking region
2098 - 4011	cc49-IL2 coding region
4068 - 4661	MoMuLV 3' LTR

Figure 14a
SEQ ID NO:11
Alpha-Lactalbumin YP Vector

1	GATCAGTCCTGGGTGGTCATTGAAAGGACTGATGCTGAAGTTGAAGCTCC
51	AATACTTTGGCCACCTGATGCGAAGAACTGACTCATGTGATAAGACCCTG
101	ATACTGGGAAAGATTGAAGGCAGGAGGAGAAGGGATGACAGAGGATGGAA
151	GAGTTGGATGGAATCACCAACTCGATGGACATGAGTTTGAGCAAGCTTCC
201	AGGAGTTGGTAATGGGCAGGGAAGCCTGGCGTGCTGCAGTCCATGGGGTT
251	GCAAAGAGTTGGACACTACTGAGTGACTGAACTGAACTGATAGTGTAATC
301	CATGGTACAGAATATAGGATAAAAAAGAGGAAGAGTTTGCCCTGATTCTG
351	AAGAGTTGTAGGATATAAAAGTTTAGAATACCTTTAGTTTGGAAGTCTTA
401	AATTATTTACTTAGGATGGGTACCCACTGCAATATAAGAAATCAGGCTTT
451	AGAGACTGATGTAGAGAGAATGAGCCCTGGCATACCAGAAGCTAACAGCT
501	ATTGGTTATAGCTGTTATAACCAATATATAACCAATATATTGGTTATATA
551	GCATGAAGCTTGATGCCAGCAATTTGAAGGAACCATTTAGAACTAGTATC
601	CTAAACTCTACATGTTCCAGGACACTGATCTTAAAGCTCAGGTTCAGAAT
651	CTTGTTTTATAGGCTCTAGGTGTATATTGTGGGGCTTCCCTGGTGGCTCA
701	GATGGTAAAGTGTCTGCCTGCAATGTGGGTGATCTGGGTTCGATCCCTGG
751	CTTGGGAAGATCCCCTGGAGAAGGAAATGGCAACCCACTCTAGTACTCTT
801	ACCTGGAAAATTCCATGGACAGAGGAGCCTTGTAAGCTACAGTCCATGGG
851	ATTGCAAAGAGTTGAACACAACTGAGCAACTAAGCACAGCACAGTACAGT
901	ATACACCTGTGAGGTGAAGTGAAGTGAAGGTTCAATGCAGGGTCTCCTGC
951	ATTGCAGAAAGATTCTTTACCATCTGAGCCACCAGGGAAGCCCAAGAATA
1001	CTGGAGTGGGTAGCCTATTCCTTCTCCAGGGGATCTTCCCATCCCAGGAA
1051	TTGAACTGGAGTCTCCTGCATTTCAGGTGGATTCTTCACCAGCTGAACTA
1101	CCAGGTGGATACTACTCCAATATTAAAGTGCTTAAAGTCCAGTTTTCCCA
1151	CCTTTCCCAAAAAGGTTGGGTCACTCTTTTTTAACCTTCTGTGGCCTACT
1201	CTGAGGCTGTCTACAAGCTTATATATTTATGAACACATTTATTGCAAGTT
1251	GTTAGTTTTAGATTTACAATGTGGTATCTGGCTATTTAGTGGTATTGGTG
1301	GTTGGGGATGGGGAGGCTGATAGCATCTCAGAGGGCAGCTAGATACTGTC
1351	ATACACACTTTTCAAGTTCTCCATTTTTGTGAAATAGAAAGTCTCTGGAT
1401	CTAAGTTATATGTGATTCTCAGTCTCTGTGGTCATATTCTATTCTACTCC
1451	TGACCACTCAACAAGGAACCAAGATATCAAGGGACACTTGTTTTGTTTCA
1501	TGCCTGGGTTGAGTGGGCCATGACATATGTTCTGGGCCTTGTTACATGGC
1551	TGGATTGGTTGGACAAGTGCCAGCTCTGATCCTGGGACTGTGGCATGTGA
1601	TGACATACACCCCCTCTCCACATTCTGCATGTCTCTAGGGGGGAAGGGGG
1651	AAGCTCGGTATAGAACCTTTATTGTATTTTCTGATTGCCTCACTTCTTAT
1701	ATTGCCCCCATGCCCTTCTTTGTTCCTCAAGTAACCAGAGACAGTGCTTC
1751	CCAGAACCAACCCTACAAGAAACAAAGGGCTAAACAAAGCCAAATGGGAA
1801	GCAGGATCATGGTTTGAACTCTTTCTGGCCAGAGAACAATACCTGCTATG
1851	GACTAGATACTGGGAGAGGGAAAGGAAAAGTAGGGTGAATTATGGAAGGA
1901	AGCTGGCAGGCTCAGCGTTTCTGTCTTGGCATGACCAGTCTCTCTTCATT
1951	CTCTTCCTAGATGTAGGGCTTGGTACCAGAGCCCCTGAGGCTTTCTGCAT
2001	GAATATAAATATATGAAACTGAGTGATGCTTCCATTTCAGGTTCTTGGGG
2051	GCGCCGAATTCGAGCTCGGTACCCGGGGATCTCGACGGATCCGATTACTT
2101	ACTGGCAGGTGCTGGGGGCTTCCGAGACAATCGCGAACATCTACACCACA
2151	CAACACCGCCTCGACCAGGGTGAGATATCGGCCGGGGACGCGGCGGTGGT
2201	AATTACAAGCGAGATCCGATTACTTACTGGCAGGTGCTGGGGGCTTCCGA
2251	GACAATCGCGAACATCTACACCACACAACACCGCCTCGACCAGGGTGAGA
2301	TATCGGCCGGGGACGCGGCGGTGGTAATTACAAGCGAGATCTCGAGTTAA
2351	CAGATCTAGGCCTCCTAGGTCGACGGATCCCCGGGAATTCGGCGCCGCCA
2401	CCATGATGTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCC
2451	ACCCAGGCCCAGGTCCAACTGCAGCAGTCTGGGCCTGAGCTGGTGAAGCC
2501	TGGGACTTCAGTGAGGATATCCTGCAAGGCTTCTGGCTACACCTTCACAA
2551	GCTACTATTTACACTGGGTGAAGCAGAGGCCTGGACAGGGACTTGAGTGG
2601	ATTGCATGGATTTATCCTGGAAATGTTATTACTACGTACAATGAGAAGTT
2651	CAAGGGCAAGGCCACACTGACTGCAGACAAATCCTCCAGCACAGCCTACA
2701	TGCACCTCAACAGCCTGACCTCTGAGGACTCTGCGGTCTATTTCTGTGCA
2751	AGGGGTGACCATGATCTTGACTACTGGGGCCAAGGCACCACTCTCACAGT
2801	CTCCTCAGCCAAAACGACACCCCCATCTGTCTATCCACTGGCCCCTGGAT

Figure 14b

```
2851  CTGCTGCCCAAACTAACTCCATGGTGACCCTGGGATGCCTGGTCAAGGGC
2901  TATTTCCCTGAGCCAGTGACAGTGACCTGGAACTCTGGATCCCTGTCCAG
2951  CGGTGTGCACACCTTCCCAGCTGTCCTGCAGTCTGACCTCTACACTCTGA
3001  GCAGCTCAGTGACTGTCCCCTCCAGCACCTGGCCCAGCGAGACCGTCACC
3051  TGCAACGTTGCCCACCCGGCCAGCAGCACCAAGGTGGACAAGAAAATTGT
3101  GCCCAGGGATTGTACTAGTGGAGGTGGAGGTAGCTAAGGGAGATCTCGAC
3151  GGATCCCCGGGAATTCGCCCCTCTCCCTCCCCCCCCCCTAACGTTACTGG
3201  CCGAAGCCGCTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTATTTT
3251  CCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCT
3301  GTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGAAT
3351  GCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTT
3401  GAAGACAAACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCCCCA
3451  CCTGGCGACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATACACC
3501  TGCAAAGGCGGCACAACCCCAGTGCCACGTTGTGAGTTGGATAGTTGTGG
3551  AAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGAT
3601  GCCCAGAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTGCAC
3651  ATGCTTTACATGTGTTTAGTCGAGGTTAAAAAAACGTCTAGGCCCCCCGA
3701  ACCACGGGGACGTGGTTTTCCTTTGAAAAACACGATGATAATATGGCCTC
3751  CTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCCG
3801  ACATTGTGCTGACACAATCTCCAGCAATCATGTCTGCATCTCCAGGGGAG
3851  AAGGTCACCATGACCTGCAGTGCCACCTCAAGTGTAAGTTACATACACTG
3901  GTACCAGCAGAAGTCAGGCACCTCCCCCAAAAGATGGATTTATGACACAT
3951  CCAAACTGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCAGTGGGTCTGGG
4001  ACCTCTCACTCTCTCACACTCAGCAGCATGGAGGCTGAAGATGCTGCCAC
4051  TTATTACTGCCAGCAGTGGGGTAGTTACCTCACGTTCGGTGCGGGGACCA
4101  AGCTGGAGCTGAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCCA
4151  CCATCCAGTGAGCAGTTAACATCTGGAGGTGCCTCAGTCGTGTGCTTCTT
4201  GAACAACTTCTACCCCAAAGACATCAATGTCAAGTGGAAGATTGATGGCA
4251  GTGAACGACAAAATGGCGTCCTGAACAGTTGGACTGATCAGGACAGCAAA
4301  GACAGCACCTACAGCATGAGCAGCACCCTCACGTTGACCAAGGACGAGTA
4351  TGAACGACATAACAGCTATACCTGTGAGGCCACTCACAAGACATCAACTT
4401  CACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTTAATAGGGGAGATCT
4451  CGACATCGATAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTG
4501  GTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTA
4551  ATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTC
4601  CTTGTATAAATCCTGGTTGCTGTCTCTTTATGAGGAGTTGTGGCCCGTTG
4651  TCAGGCAACGTGGCGTGGTGTGCACTGTGTTTGCTGACGCAACCCCCACT
4701  GGTTGGGGCATTGCCACCACCTGTCAGCTCCTTTCCGGGACTTTCGCTTT
4751  CCCCCTCCCTATTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCT
4801  GCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGTGTTGTCG
4851  GGGAAATCATCGTCCTTTCCTTGGCTGCTCGCCTGTGTTGCCACCTGGAT
4901  TCTGCGCGGGACGTCCTTCTGCTACGTCCCTTCGGCCCTCAATCCAGCGG
4951  ACCTTCCTTCCCGCGGCCTGCTGCCGGCTCTGCGGCCTCTTCCGCGTCTT
5001  CGCCTTCGCCCTCAGACGAGTCGGATCTCCCTTTGGGCCGCCTCCCCGCC
5051  TGATCGATAAAATAAAAGATTTTATTTAGTCTCCAGAAAAAGGGGGGAAT
5101  GAAAGACCCCACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTT
5151  GCAAGGCATGGAAAAATACATAACTGAGAATAGAGAAGTTCAGATCAAGG
5201  TCAGGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGT
5251  AAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAAT
5301  ATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGG
5351  CCAAGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGA
5401  GAACCATCAGATGTTTCCAGGGTGCCCCAAGGACCTGAAATGACCCTGTG
5451  CCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCT
5501  TCTGCTCCCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGGGCGC
5551  CAGTCCTCCGATTGACTGAGTCGCCCGGGTACCCGTGTATCCAATAAACC
5601  CTCTTGCAGTTGCATCCGACTTGTGGTCTCGCTGTTCCTTGGGAGGGTCT
```

Figure 14c

5651 CCTCTGAGTGATTGACTACCCGTCAGCGGGGGTCTTTCATT

1 - 2053	Bovine/Human Alpha-lactalbumin 5' flanking region
2093 - 2336	Double mutated PPE sequence
2403 - 2459	Bovine alpha-lactalbumin signal peptide coding region
2460 - 3137	Yersenia pestis heavy chain Fab gene coding region
3167 - 3742	EMCV IRES
3743 - 3799	Bovine alpha-lactalbumin signal peptide coding region
3800 - 4441	Yersenia pestis light chain Fab gene coding region
4461 - 5052	WPRE sequence
5098 - 5691	Moloney murine leukemia virus 3' LTR

Figure 15
SEQ ID NO:12
IRES-Casein Signal Peptide Sequence

```
1     GGAATTCGCCCCTCTCCCTCCCCCCCCCCTAACGTTACTGGCCGAAGCCG
51    CTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTATTTTCCACCATAT
101   TGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCTGTCTTCTTG
151   ACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGAATGCAAGGTCT
201   GTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAAA
251   CAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCCCCACCTGGCGAC
301   AGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAAGGC
351   GGCACAACCCCAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGAGTCA
401   AATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCCAGAAG
451   GTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTGCACATGCTTTAC
501   ATGTGTTTAGTCGAGGTTAAAAAAACGTCTAGGCCCCCCGAACCACGGGG
551   ACGTGGTTTTCCTTTGAAAAACACGATGATAATATGGCCTTGCTCATCCT
601   TACCTGTCTTGTGGCTGTTGCTCTTGCCGGCGCCATGGGATATCTAGATC
651   TCGAGCTCGCGAAAGCTT
```

1 - 583	IRES
584 - 628	Modified bovine alpha-S1 casein signal peptide coding region
629 - 668	Multiple cloning site

Figure 16a

SEQ ID NO: 13

LNBOTDC Vector

```
   1  TTTGAAAGACCCCACCCGTAGGTGGCAAGCTAGCTTAAGTAACGCCACTT
  51  TGCAAGGCATGGAAAAATACATAACTGAGAATAGAAAAGTTCAGATCAAG
 101  GTCAGGAACAAAGAAACAGCTGAATACCAAACAGGATATCTGTGGTAAGC
 151  GGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGAGACAGCTGAGTGATG
 201  GGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCGGGGCCA
 251  AGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGTGAA
 301  TCATCAGATGTTTCCAGGGTGCCCCAAGGACCTGAAAATGACCCTGTACC
 351  TTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCTTC
 401  CGCTCTCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGCGCGCCA
 451  GTCTTCCGATAGACTGCGTCGCCCGGGTACCCGTATTCCCAATAAAGCCT
 501  CTTGCTGTTTGCATCCGAATCGTGGTCTCGCTGTTCCTTGGGAGGGTCTC
 551  CTCTGAGTGATTGACTACCCACGACGGGGGTCTTTCATTTGGGGGCTCGT
 601  CCGGGATTTGGAGACCCCTGCCCAGGGACCACCGACCCACCACCGGGAGG
 651  TAAGCTGGCCAGCAACTTATCTGTGTCTGTCCGATTGTCTAGTGTCTATG
 701  TTTGATGTTATGCGCCTGCGTCTGTACTAGTTAGCTAACTAGCTCTGTAT
 751  CTGGCGGACCCGTGGTGGAACTGACGAGTTCTGAACACCCGGCCGCAACC
 801  CTGGGAGACGTCCCAGGGACTTTGGGGGCCGTTTTTGTGGCCCGACCTGA
 851  GGAAGGGAGTCGATGTGGAATCCGACCCCGTCAGGATATGTGGTTCTGGT
 901  AGGAGACGAGAACCTAAAACAGTTCCCGCCTCCGTCTGAATTTTTGCTTT
 951  CGGTTTGGAACCGAAGCCGCGCGTCTTGTCTGCTGCAGCGCTGCAGCATC
1001  GTTCTGTGTTGTCTCTGTCTGACTGTGTTTCTGTATTTGTCTGAAAATTA
1051  GGGCCAGACTGTTACCACTCCCTTAAGTTTGACCTTAGGTCACTGGAAAG
1101  ATGTCGAGCGGATCGCTCACAACCAGTCGGTAGATGTCAAGAAGAGACGT
1151  TGGGTTACCTTCTGCTCTGCAGAATGGCCAACCTTTAACGTCGGATGGCC
1201  GCGAGACGGCACCTTTAACCGAGACCTCATCACCCAGGTTAAGATCAAGG
1251  TCTTTTCACCTGGCCCGCATGGACACCCAGACCAGGTCCCCTACATCGTG
1301  ACCTGGGAAGCCTTGGCTTTTGACCCCCCTCCCTGGGTCAAGCCCTTTGT
1351  ACACCCTAAGCCTCCGCCTCCTCTTCCTCCATCCGCCCCGTCTCTCCCCC
1401  TTGAACCTCCTCGTTCGACCCCGCCTCGATCCTCCCTTTATCCAGCCCTC
1451  ACTCCTTCTCTAGGCGCCGGAATTCCGATCTGATCAAGAGACAGGATGAG
1501  GATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCC
1551  GCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGG
1601  CTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTC
1651  TTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAGGACGAG
1701  GCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGT
1751  GCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAG
1801  TGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTA
1851  TCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTAC
1901  CTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTC
1951  GGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAG
2001  GGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGA
2051  CGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCA
2101  TGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGT
2151  GTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGA
2201  AGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCG
2251  CCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTC
2301  TTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAAC
2351  CTGCCATCACGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGG
2401  CTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGG
2451  ATCTCATGCTGGAGTTCTTCGCCCACCCCGGGCTCGATCCCCTCGCGAGT
2501  TGGTTCAGCTGCTGCCTGAGGCTGGACGACCTCGCGGAGTTCTACCGGCA
2551  GTGCAAATCCGTCGGCATCCAGGAAACCAGCAGCGGCTATCCGCGCATCC
2601  ATGCCCCCGAACTGCAGGAGTGGGGAGGCACGATGGCCGCTTTGGTCGAG
2651  GCGGATCCGGCCATTAGCCATATTATTCATTGGTTATATAGCATAAATCA
2701  ATATTGGCTATTGGCCATTGCATACGTTGTATCCATATCATAATATGTAC
2751  ATTTATATTGGCTCATGTCCAACATTACCGCCATGTTGACATTGATTATT
```

Figure 16b

2801 GACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCAT
2851 ATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGA
2901 CCGCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCAT
2951 AGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTAC
3001 GGTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACG
3051 CCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCA
3101 GTACATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAG
3151 TCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGT
3201 GGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGT
3251 CAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTC
3301 GTAACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCATGTACGGTGG
3351 GAGGTCTATATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCGCCTGGAG
3401 ACGCCATCCACGCTGTTTTGACCTCCATAGAAGACACCGGGACCGATCCA
3451 GCCTCCGCGGCCCCAAGCTTCTCGACGGATCCCCGGGAATTCAGGCCATC
3501 GATCCCGCCGCCACCATGGAATGGAGCTGGGTCTTTCTCTTCTTCCTGTC
3551 AGTAACTACAGGTGTCCACTCCGACATCCAGATGACCCAGTCTCCAGCCT
3601 CCCTATCTGCATCTGTGGGAGAAACTGTCACTATCACATGTCGAGCAAGT
3651 GGGAATATTCACAATTATTTAGCATGGTATCAGCAGAAACAGGGAAAATC
3701 TCCTCAGCTCCTGGTCTATAATGCAAAAACCTTAGCAGATGGTGTGCCAT
3751 CAAGGTTCAGTGGCAGTGGATCAGGAACACAATATTCTCTCAAGATCAAC
3801 AGCCTGCAGCCTGAAGATTTTGGGAGTTATTACTGTCAACATTTTTGGAG
3851 TACTCCGTGGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAACGGGCTG
3901 ATGCTGCACCAACTGTATCCATCTTCCCACCATCCAGTGAGCAGTTAACA
3951 TCTGGAGGTGCCTCAGTCGTGTGCTTCTTGAACAACTTCTACCCCAAAGA
4001 CATCAATGTCAAGTGGAAGATTGATGGCAGTGAACGACAAAATGGCGTCC
4051 TGAACAGTTGGACTGATCAGGACAGCAAAGACAGCACCTACAGCATGAGC
4101 AGCACCCTCACATTGACCAAGGACGAGTATGAACGACATAACAGCTATAC
4151 CTGTGAGGCCACTCACAAGACATCAACTTCACCCATTGTCAAGAGCTTCA
4201 ACAGGAATGAGTGTTGAAAGCATCGATTTCCCCTGAATTCGCCCCTCTCC
4251 CTCCCCCCCCCCTAACGTTACTGGCCGAAGCCGCTTGGAATAAGGCCGGT
4301 GTGCGTTTGTCTATATGTTATTTTCCACCATATTGCCGTCTTTTGGCAAT
4351 GTGAGGGCCCGGAAACCTGGCCCTGTCTTCTTGACGAGCATTCCTAGGGG
4401 TCTTTCCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGTCGTGAAGG
4451 AAGCAGTTCCTCTGGAAGCTTCTTGAAGACAAACAACGTCTGTAGCGACC
4501 CTTTGCAGGCAGCGGAACCCCCCACCTGGCGACAGGTGCCTCTGCGGCCA
4551 AAAGCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCCAGTGCC
4601 ACGTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGC
4651 GTATTCAACAAGGGGCTGAAGGATGCCCAGAAGGTACCCCATTGTATGGG
4701 ATCTGATCTGGGGCCTCGGTGCACATGCTTTACATGTGTTTAGTCGAGGT
4751 TAAAAAAACGTCTAGGCCCCCCGAACCACGGGGACGTGGTTTTCCTTTGA
4801 AAAACACGATGATAATATGGCCTCCTTTGTCTCTCTGCTCCTGGTAGGCA
4851 TCCTATTCCATGCCACCCAGGCCGAGGTTCAGCTTCAGCAGTCTGGGGCA
4901 GAGCTTGTGAAGCCAGGGGCCTCAGTCAAGTTGTCCTGCACAGCTTCTGG
4951 CTTCAACATTAAAGACACCTTTATGCACTGGGTGAAGCAGAGGCCTGAAC
5001 AGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAATGGGAATACTGAA
5051 TATGACCCGAAGTTCCAGGGCAAGGCCACTATAACAGCAGACACATCCTC
5101 CAACACAGTCAACCTGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCG
5151 TCTATTACTGTGCTAGTGGAGGGGAACTGGGGTTTCCTTACTGGGGCCAA
5201 GGGACTCTGGTCACTGTCTCTGCAGCCAAAACGACACCCCCATCTGTCTA
5251 TCCACTGGCCCCTGGATCTGCTGCCCAAACTAACTCCATGGTGACCCTGG
5301 GATGCCTGGTCAAGGGCTATTTCCCTGAGCCAGTGACAGTGACCTGGAAC
5351 TCTGGATCCCTGTCCAGCGGTGTGCACACCTTCCCAGCTGTCCTGCAGTC
5401 TGACCTCTACACTCTGAGCAGCTCAGTGACTGTCCCCTCCAGCACCTGGC
5451 CCAGCGAGACCGTCACCTGCAACGTTGCCCACCCGGCCAGCAGCACCAAG
5501 GTGGACAAGAAAATTGTGCCCAGGGATTGTACTAGTGGAGGTGGAGGTAG
5551 CCACCATCACCATCACCATTAATCTAGAGTTAAGCGGCCGTCGAGATCTA
5601 GGCCTCCTAGGTCGACATCGATAAAATAAAAGATTTTATTTAGTCTCCAG
5651 AAAAAGGGGGGAATGAAAGACCCCACCTGTAGGTTTGGCAAGCTAGCTTA
5701 AGTAACGCCATTTTGCAAGGCATGGAAAAATACATAACTGAGAATAGAGA
5751 AGTTCAGATCAAGGTCAGGAACAGATGGAACAGCTGAATATGGGCCAAAC
5801 AGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGA
5851 TGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCT

Figure 16c

```
5901  GCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCAGCCCT
5951  CAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAAGGACCT
6001  GAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCT
6051  TCTGTTCGCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCCACAACCC
6101  CTCACTCGGGGCGCCAGTCCTCCGATTGACTGAGTCGCCCGGGTACCCGT
6151  GTATCCAATAAACCCTCTTGCAGTTGCATCCGACTTGTGGTCTCGCTGTT
6201  CCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGGGGTCTT
      TCATT
```

Moloney Murine Sarcoma Virus 5' LTR	1 - 589
Moloney Murine Leukemia Virus Extended Packaging Region	659 - 1468
Neomycin Resistance Gene	1512 - 2306
CMV Promoter	2656 - 3473
cc49 Signal Peptide Coding Region	3516 - 3572
Bot Fab 5 Light Chain	3573 - 4217
EMCV IRES (Clonetech)	4235 - 4816
Modified Bovine α-LA Signal Peptide Coding Region	4817 - 4873
Bot Fab 5 Heavy Chain	4874 - 5572
Moloney Murine Leukemia Virus 3' LTR	5662 - 6255

Figure 17a
SEQ ID NO: 34
LNBOTDC Vector

```
   1 GAATTAATTCATACCAGATCACCGAAAACTGTCCTCCAAATGTGTCCCCC
  51 TCACACTCCCAAATTCGCGGGCTTCTGCCTCTTAGACCACTCTACCCTAT
 101 TCCCCACACTCACCGGAGCCAAAGCCGCGGCCCTTCCGTTTCTTTGCTTT
 151 TGAAAGACCCCACCCGTAGGTGGCAAGCTAGCTTAAGTAACGCCACTTTG
 201 CAAGGCATGGAAAAATACATAACTGAGAATAGAAAAGTTCAGATCAAGGT
 251 CAGGAACAAAGAAACAGCTGAATACCAAACAGGATATCTGTGGTAAGCGG
 301 TTCCTGCCCCGGCTCAGGGCCAAGAACAGATGAGACAGCTGAGTGATGGG
 351 CCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCGGGGCCAAG
 401 AACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGTGAATC
 451 ATCAGATGTTTCCAGGGTGCCCCAAGGACCTGAAAATGACCCTGTACCTT
 501 ATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCTTCCG
 551 CTCTCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGCGCGCCAGT
 601 CTTCCGATAGACTGCGTCGCCCGGGTACCCGTATTCCCAATAAAGCCTCT
 651 TGCTGTTTGCATCCGAATCGTGGTCTCGCTGTTCCTTGGGAGGGTCTCCT
 701 CTGAGTGATTGACTACCCACGACGGGGGTCTTTCATTTGGGGGCTCGTCC
 751 GGGATTTGGAGACCCCTGCCCAGGGACCACCGACCCACCACCGGGAGGTA
 801 AGCTGGCCAGCAACTTATCTGTGTCTGTCCGATTGTCTAGTGTCTATGTT
 851 TGATGTTATGCGCCTGCGTCTGTACTAGTTAGCTAACTAGCTCTGTATCT
 901 GGCGGACCCGTGGTGGAACTGACGAGTTCTGAACACCCGGCCGCAACCCT
 951 GGGAGACGTCCCAGGGACTTTGGGGGCCGTTTTTGTGGCCCGACCTGAGG
1001 AAGGGAGTCGATGTGGAATCCGACCCCGTCAGGATATGTGGTTCTGGTAG
1051 GAGACGAGAACCTAAAACAGTTCCCGCCTCCGTCTGAATTTTTGCTTTCG
1101 GTTTGGAACCGAAGCCGCGCGTCTTGTCTGCTGCAGCGCTGCAGCATCGT
1151 TCTGTGTTGTCTCTGTCTGACTGTGTTTCTGTATTTGTCTGAAAATTAGG
1201 GCCAGACTGTTACCACTCCCTTAAGTTTGACCTTAGGTCACTGGAAAGAT
1251 GTCGAGCGGATCGCTCACAACCAGTCGGTAGATGTCAAGAAGAGACGTTG
1301 GGTTACCTTCTGCTCTGCAGAATGGCCAACCTTTAACGTCGGATGGCCGC
1351 GAGACGGCACCTTTAACCGAGACCTCATCACCCAGGTTAAGATCAAGGTC
1401 TTTTCACCTGGCCCGCATGGACACCCAGACCAGGTCCCCTACATCGTGAC
1451 CTGGGAAGCCTTGGCTTTTGACCCCCCTCCCTGGGTCAAGCCCTTTGTAC
1501 ACCCTAAGCCTCCGCCTCCTCTTCCTCCATCCGCCCCGTCTCTCCCCCTT
1551 GAACCTCCTCGTTCGACCCCGCCTCGATCCTCCCTTTATCCAGCCCTCAC
1601 TCCTTCTCTAGGCGCCGGAATTCCGATCTGATCAAGAGACAGGATGAGGG
1651 AGCTTGTATATCCATTTTCGGATCTGATCAGCACGTGTTGACAATTAATC
1701 ATCGGCATAGTATATCGGCATAGTATAATACGACAAGGTGAGGAACTAAA
1751 CCATGGCCAAGCCTTTGTCTCAAGAAGAATCCACCCTCATTGAAAGAGCA
1801 ACGGCTACAATCAACAGCATCCCCATCTCTGAAGACTACAGCGTCGCCAG
1851 CGCAGCTCTCTCTAGCGACGGCCGCATCTTCACTGGTGTCAATGTATATC
1901 ATTTTACTGGGGGACCTTGTGCAGAACTCGTGGTGCTGGGCACTGCTGCT
1951 GCTGCGGCAGCTGGCAACCTGACTTGTATCGTCGCGATCGGAAATGAGAA
2001 CAGGGGCATCTTGAGCCCCTGCGGACGGTGTCGACAGGTGCTTCTCGATC
2051 TGCATCCTGGGATCAAAGCGATAGTGAAGGACAGTGATGGACAGCCGACG
2101 GCAGTTGGGATTCGTGAATTGCTGCCCTCTGGTTATGTGTGGGAGGGCTA
2151 AGCACTTCGTGGCCGAGGAGCAGGACTGACACGTGCTACGAGATTTCGAT
2201 TCCACCGCCGCCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGA
2251 CGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCG
2301 CCCACCCCAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAAT
2351 AGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTG
2401 TGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGTACGAGTTGGT
2451 TCAGCTGCTGCCTGAGGCTGGACGACCTCGCGGAGTTCTACCGGCAGTGC
2501 AAATCCGTCGGCATCCAGGAAACCAGCAGCGGCTATCCGCGCATCCATGC
2551 CCCCGAACTGCAGGAGTGGGGAGGCACGATGGCCGCTTTGGTCGAGGCGG
2601 ATCCGGCCATTAGCCATATTATTCATTGGTTATATAGCATAAATCAATAT
2651 TGGCTATTGGCCATTGCATACGTTGTATCCATATCATAATATGTACATTT
2701 ATATTGGCTCATGTCCAACATTACCGCCATGTTGACATTGATTATTGACT
2751 AGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATAT
2801 GGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACCGC
2851 CCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTA
```

Figure 17b

```
2901  ACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTA
2951  AACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCC
3001  CTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTAC
3051  ATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCAT
3101  CGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGAT
3151  AGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCAAT
3201  GGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAA
3251  CAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCATGTACGGTGGGAGG
3301  TCTATATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCGCCTGGAGACGC
3351  CATCCACGCTGTTTTGACCTCCATAGAAGACACCGGGACCGATCCAGCCT
3401  CCGCGGCCCCAAGCTTCTCGAGTTAACAGATCTAGGCTGGCACGACAGGT
3451  TTCCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTAG
3501  CTCACTCATTAGGCACCCCAGGCTTTACACTTTATGCTTCCGGCTCGTAT
3551  GTTGTGTGGAATTGTGAGCGGATAACAATTTCACACAGGAAACAGCTATG
3601  ACCATGATTACGCCAAGCTTGGCTGCAGGTCGACGGATCCACTAGTAACG
3651  GCCGCCAGTGTGCTGGAATTCACCATGGGGCAACCCGGGAACGGCAGCGC
3701  CTTCTTGCTGGCACCCAATGGAAGCCATGCGCCGGACCACGACGTCACGC
3751  AGCAAAGGGACGAGGTGTGGGTGGTGGGCATGGGCATCGTCATGTCTCTC
3801  ATCGTCCTGGCCATCGTGTTTGGCAATGTGCTGGTCATCACAGCCATTGC
3851  CAAGTTCGAGCGTCTGCAGACGGTCACCAACTACTTCATCACAAGCTTGG
3901  CCTGTGCTGATCTGGTCATGGGGCTAGCAGTGGTGCCCTTTGGGGCCGCC
3951  CATATTCTCATGAAAATGTGGACTTTTGGCAACTTCTGGTGCGAGTTCTG
4001  GACTTCCATTGATGTGCTGTGCGTCACGGCATCGATTGAGACCCTGTGCG
4051  TGATCGCAGTCGACCGCTACTTTGCCATTACTAGTCCTTTCAAGTACCAG
4101  AGCCTGCTGACCAAGAATAAGGCCCGGGTGATCATTCTGATGGTGTGGAT
4151  TGTGTCAGGCCTTACCTCCTTCTTGCCCATTCAGATGCACTGGTACAGGG
4201  CCACCCACCAGGAAGCCATCAACTGCTATGCCAATGAGACCTGCTGTGAC
4251  TTCTTCACGAACCAAGCCTATGCCATTGCCTCTTCCATCGTGTCCTTCTA
4301  CGTTCCCCTGGTGATCATGGTCTTCGTCTACTCCAGGGTCTTTCAGGAGG
4351  CCAAAAGGCAGCTCCAGAAGATTGACAAATCTGAGGGCCGCTTCCATGTC
4401  CAGAACCTTAGCCAGGTGGAGCAGGATGGGCGGACGGGGCATGGACTCCG
4451  CAGATCTTCCAAGTTCTGCTTGAAGGAGCACAAAGCCCTCAAGACGTTAG
4501  GCATCATCATGGGCACTTTCACCCTCTGCTGGCTGCCCTTCTTCATCGTT
4551  AACATTGTGCATGTGATCCAGGATAACCTCATCCGTAAGGAAGTTTACAT
4601  CCTCCTAAATTGGATAGGCTATGTCAATTCTGGTTTCAATCCCCTTATCT
4651  ACTGCCGGAGCCCAGATTTCAGGATTGCCTTCCAGGAGCTTCTGTGCCTG
4701  CGCAGGTCTTCTTTGAAGGCCTATGGCAATGGCTACTCCAGCAACGGCAA
4751  CACAGGGGAGCAGAGTGGATATCACGTGGAACAGGAGAAAGAAAATAAAC
4801  TGCTGTGTGAAGACCTCCCAGGCACGGAAGACTTTGTGGGCCATCAAGGT
4851  ACTGTGCCTAGCGATAACATTGATTCACAAGGGAGGAATTGTAGTACAAA
4901  TGACTCACTGCTCTCGAGAATCGAGGGGCGGCACCACCATCATCACCACG
4951  TCGACCCCGGGGACTACAAGGATGACGATGACAAGTAAGCTTTATCCATC
5001  ACACTGGCGGCCGCTCGAGCATGCATCTAGCGGCCGCTCGAGGCCGGCAA
5051  GGCCGGATCCCCGGGAATTCGCCCCTCTCCCTCCCCCCCCCCTAACGTTA
5101  CTGGCCGAAGCCGCTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTA
5151  TTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGG
5201  CCCTGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAG
5251  GAATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCT
5301  TCTTGAAGACAAACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCC
5351  CCCACCTGGCGACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATA
5401  CACCTGCAAAGGCGGCACAACCCCAGTGCCACGTTGTGAGTTGGATAGTT
5451  GTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAA
5501  GGATGCCCAGAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGT
5551  GCACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAAACGTCTAGGCCCC
5601  CCGAACCACGGGGACGTGGTTTTCCTTTGAAAAACACGATGATAATATGG
5651  CCTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAG
5701  GCCGAGCTCACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAG
5751  GGCCACCATCAACTGCAAGTCCAGCCAGAGTGTTTTGTACAGCTCCAACA
5801  ATAAGAACTATTTAGCTTGGTATCAGCAGAAACCAGGACAGCCTCCTAAG
5851  CTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATT
5901  CAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGC
5951  AGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACTCAG
```

Figure 17c

```
6001  ACGTTCGGCCAAGGGACCAAGGTGGAAATCAAACGAACTGTGGCTGCACC
6051  ATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTG
6101  CCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTA
6151  CAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGT
6201  CACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGA
6251  CGCTGAGCAAAGCAGACTACGAGAAACACAAACTCTACGCCTGCGAAGTC
6301  ACCCATCAGGGCCTGAGATCGCCCGTCACAAAGAGCTTCAACAAGGGGAG
6351  AGTGTTAGTTCTAGATAATTAATTAGGAGGAGATCTCGAGCTCGCGAAAG
6401  CTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCG
6451  TTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCCTCCTA
6501  GGTCGACATCGATAAAATAAAAGATTTTATTTAGTCTCCAGAAAAAGGGG
6551  GGAATGAAAGACCCCACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCC
6601  ATTTTGCAAGGCATGGAAAAATACATAACTGAGAATAGAGAAGTTCAGAT
6651  CAAGGTCAGGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCT
6701  GTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGAACAGC
6751  TGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCT
6801  CAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTT
6851  CTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAAGGACCTGAAATGACC
6901  CTGTGCCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGC
6951  GCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGG
7001  GGCGCCAGTCCTCCGATTGACTGAGTCGCCCGGGTACCCGTGTATCCAAT
7051  AAACCCTCTTGCAGTTGCATCCGACTTGTGGTCTCGCTGTTCCTTGGGAG
7101  GGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGGGGTCTTTCATTTGGG
7151  GGCTCGTCCGGGATCGGGAGACCCCTGCCCAGGGACCACCGACCCACCAC
7201  CGGGAGGTAAGCTGGCTGCCTCGCGCGTTTCGGTGATGACGGTGAAAACC
7251  TCTGACACATGCAGCTCCCGGAGACGGTCACAGCTTGTCTGTAAGCGGAT
7301  GCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTG
7351  TCGGGGCGCAGCCATGACCCAGTCACGTAGCGATAGCGGAGTGTATACTG
7401  GCTTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGC
7451  GGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGC
7501  TCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCG
7551  GCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAAT
7601  CAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCC
7651  AGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCC
7701  CCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACC
7751  CGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTG
7801  CGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCT
7851  CCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCA
7901  GTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCC
7951  GTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAA
8001  CCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGA
8051  TTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGG
8101  CCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCT
8151  GAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAC
8201  AAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACG
8251  CGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTC
8301  TGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGAT
8351  TATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTT
8401  AAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATG
8451  CTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTCGTTCATCCA
8501  TAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTA
8551  CCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACCGGC
8601  TCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAA
8651  GTGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGG
8701  GAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGC
8751  CATTGCTGCAGGCATCGTGGTGTCACGCTCGTCGTTTGGTATGGCTTCAT
8801  TCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTG
8851  TGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAA
8901  GTTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTC
8951  TTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCA
9001  ACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCC
9051  GGCGTCAACACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGC
```

APPROVED O.G. FIG.
BY CLASS SUBCLASS
DRAFTSMAN

Figure 17d

9101 TCATCATTGGAAAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCG
9151 CTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTC
9201 AGCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGC
9251 AAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTC
9301 ATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCT
9351 CATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGG
9401 TTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATT
9451 ATTATCATGACATTAACCTATAAAAATAGGCGTATCACGAGGCCCTTTCG
1. TCTTCAAGAAT

Features:
149-737 Moloney murine sarcoma virus 5' LTR
807-1616 Extended Packaging Region
1680-1735 EM7 promoter (bacteriophage T7 promoter)
1754-2151 Blasticidin resistance gene coding sequence
2310-2440 SV40 poly A signal and site
2603-3420 CMV IE promoter
3675-4988 G-protein-coupled receptor (GPCR)
5071-5646 IRES
5647-5703 Bovine a-lactalbumin signal peptide
5704-6372 'humanized' antibody light chain
6553-7146 MoMuLV 3' LTR
7683Origin of replication
9302-8442 b-Lactmase coding sequence